(57) Abrégé/Abstract:
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Abstract

According to the invention, there is provided a novel soybean variety designated XB14H11. This invention thus relates to the seeds of soybean variety XB14H11, to the plants of soybean XB14H11 to plant parts of soybean variety XB14H11 and to methods for producing a soybean plant produced by crossing plants of the soybean variety XB14H11 with another soybean plant, using XB14H11 as either the male or the female parent.
HIGH YIELDING SOYBEAN VARIETY XB14H11

FIELD OF INVENTION

This invention relates generally the field of soybean breeding, specifically relating to a high yielding soybean variety designated XB14H11

BACKGROUND

The present invention relates to a new and distinctive soybean variety designated XB14H11, which has been the result of years of careful breeding and selection in a comprehensive soybean breeding program. There are numerous steps involving significant technical human intervention in the development of any novel, desirable plant germplasm. Plant breeding begins with the analysis and definition of problems and weaknesses of the current germplasm, the establishment of program goals, and the definition of specific breeding objectives. The next step is selection of germplasm that possess the traits to meet the program goals. The goal is to combine in a single variety an improved combination of desirable traits from the parental germplasm. These important traits may include, but are not limited to higher seed yield, resistance to diseases and/or insects, tolerance to drought and/or heat, altered fatty acid profile(s), abiotic stress tolerance, improvements in compositional traits, and better agronomic characteristics.

These processes, which lead to the final step of marketing and distribution, can take from six to twelve years of significant technical human intervention starting from the time the first cross is made. Therefore, development of new varieties is a time-consuming process that requires precise forward planning, efficient use of resources, and a minimum of changes in direction. The development of a new variety typically involves the coordinated effort of a team of scientists, including plant breeders, molecular biologists, plant pathologists, entomologists, agronomists, biochemists, bioinformaticians, market analysts, and automation specialists.
Soybean (*Glycine max*) is an important and valuable field crop. Thus, a continuing goal of soybean breeders is to develop stable, high yielding soybean varieties that are agronomically sound. The reasons for this goal are to maximize the amount of grain produced on the land used and to supply food for both animals and humans. To accomplish this goal, the soybean breeder must select and develop soybean plants that have the traits that result in superior varieties.

Pioneer soybean research scientists develop over 500,000 potential new varieties each year. Of those new varieties, 40-65 are actually selected for commercial use.

The soybean is the world’s leading source of vegetable oil and protein meal. The oil extracted from soybeans is used for cooking oil, margarine, and salad dressings. Soybean oil is composed of saturated, monounsaturated, and polyunsaturated fatty acids. It has a typical composition of 11% palmitic, 4% stearic, 25% oleic, 50% linoleic, and 9% linolenic fatty acid content ("Economic Implications of Modified Soybean Traits Summary Report", Iowa Soybean Promotion Board & American Soybean Association Special Report 92S, May 1990). Changes in fatty acid composition for improved oxidative stability and nutrition are also important traits. Industrial uses for processed soybean oil include ingredients for paints, plastics, fibers, detergents, cosmetics, and lubricants. Soybean oil may be split, inter-esterified, sulfurized, epoxidized, polymerized, ethoxylated, or cleaved. Designing and producing soybean oil derivatives with improved functionality, oliochemistry, is a rapidly growing field. The typical mixture of triglycerides is usually split and separated into pure fatty acids, which are then combined with petroleum-derived alcohols or acids, nitrogen, sulfonates, chlorine, or with fatty alcohols derived from fats and oils.

Soybean is also used as a food source for both animals and humans. Soybean is widely used as a source of protein for animal feeds for poultry, swine, and cattle. During processing of whole soybeans, the fibrous hull is removed and the oil is extracted. The remaining soybean meal is a combination of carbohydrates and approximately 50% protein.
For human consumption soybean meal is made into soybean flour which is processed to protein concentrates used for meat extenders or specialty pet foods. Production of edible protein ingredients from soybean offers healthy, less expensive replacements for animal protein in meats as well as dairy-type products.

SUMMARY

According to the invention, there is provided a novel soybean variety designated XB14H11. This invention thus relates to the seeds of soybean variety XB14H11, to the plants of soybean XB14H11, to plant parts of soybean variety XB14H11 and to methods for producing a soybean plant produced by crossing soybean variety XB14H11 with another soybean plant, using XB14H11 as either the male or the female parent. This invention also relates to methods for introgressing a transgenic or mutant trait into soybean variety XB14H11 and to the soybean plants and plant parts produced by those methods. This invention also relates to soybean varieties or breeding varieties and plant parts derived from soybean variety XB14H11, to methods for producing other soybean varieties or plant parts derived from soybean variety XB14H11 and to the soybean plants, varieties, and their parts derived from use of those methods. This invention further relates to soybean seeds, plants, and plant parts produced by crossing the soybean variety XB14H11 with another soybean variety.

An aspect of the invention is to provide a plant cell from a soybean plant designated variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein soybean variety XB14H11 comprises a first transgene conferring glyphosate resistance. The plant cell can be a seed cell. The plant cell can further comprise a second transgene. Also provided is a plant cell from a plant tissue culture produced from protoplasts or regenerable cells from the plant cell above.

Another aspect of the invention is to provide a plant cell from a soybean plant, or a plant cell from a part of the soybean plant, wherein the soybean plant
is produced by growing seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632.

Another aspect of the invention is to provide a plant cell from a soybean plant or soybean seed which is a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions.

Another aspect of the invention is to provide a plant cell from a soybean plant or soybean seed which is a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11.

Another aspect of the invention is to provide a plant cell from a descendant of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant comprises heterozygous alleles of variety XB14H11. The plant cell of can be a seed cell.

Another aspect of the invention is to provide a plant cell from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein XB14H11 comprises a first transgene conferring glyphosate resistance, and wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, and wherein the descendant or subline further comprises a second transgene.

Another aspect of the invention is to provide a plant cell from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein
XB14H11 comprises a first transgene conferring glyphosate resistance, and wherein the descendant or subline is essentially derived from soybean variety XB14H11, and wherein the descendant or subline further comprises a second transgene.

Another aspect of the invention is to provide a plant cell from a soybean plant, or a plant cell from a part of the soybean plant, wherein the plant expresses all the physiological and morphological characteristics of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632.

Another aspect of the invention is to provide an F1 plant cell from an F1 soybean plant, or a plant cell from a part of the F1 soybean plant, wherein the F1 soybean plant is the product of a cross between a first parent and a second parent, wherein either the first parent or second parent is a plant from soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, and wherein the F1 comprises heterozygous alleles of variety XB14H11.

Another aspect of the invention is to provide the use of a soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to breed a soybean plant.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to breed a soybean plant.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to breed a soybean plant.
Another aspect of the invention is to provide the use of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 as a recipient of a conversion locus.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, as a recipient of a conversion locus.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, as a recipient of a conversion locus.

Another aspect of the invention is to provide the use of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to cross with another soybean plant.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to cross with another soybean plant.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to cross with another soybean plant.
Another aspect of the invention is to provide the use of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 and comprising a first transgene for glyphosate resistance, to introduce a second transgene.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 and comprising a first transgene for glyphosate resistance, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to introduce a second transgene.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 and comprising a first transgene for glyphosate resistance, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to introduce a second transgene.

Another aspect of the invention is to provide the use of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, for oil or protein production.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, for oil or protein production.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the
descendant or subline is essentially derived from soybean variety XB14H11, for oil or protein production.

Another aspect of the invention is to provide the use of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to grow a crop.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to grow a crop.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to grow a crop.

Another aspect of the invention is to provide the crushed non-viable soybean seeds from soybean variety XB14H11, seeds of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632.

Another aspect of the invention is to provide crushed non-viable soybean seeds from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions.

Another aspect of the invention is to provide crushed non-viable soybean seeds from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-
11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11.

Another aspect of the invention is to provide the use of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to produce a genetic marker profile. The genetic marker profile can be used for marker assisted selection.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to produce a genetic marker profile. The genetic marker profile can be used for marker assisted selection.

Another aspect of the invention is to provide the use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to produce a genetic marker profile. The genetic marker profile can be used for marker assisted selection.

Definitions

Certain definitions used in the specification are provided below. Also in the examples which follow, a number of terms are used. In order to provide a clear and consistent understanding of the specification and claims, the following definitions are provided:

AERBLT = AWB = AERIAL WEB BLIGHT. Aerial web blight is caused by the fungus *Rhizoctonia solani*, which can also cause seedling blight and root rot. Stems, flowers, pods, petioles, and leaves are susceptible to formation of lesions. Tolerance to Aerial Web Blight is rated on a scale of 1 to 9, with a score
of 1 being very susceptible, ranging up to a score of 9 being tolerant. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

ALLELE. Any of one or more alternative forms of a genetic sequence. In a diploid cell or organism, the two alleles of a given sequence typically occupy corresponding loci on a pair of homologous chromosomes.

ANTHESSIS. The time of a flower's opening.

APHID ANTIBIOSIS. Aphid antibiosis is the ability of a variety to reduce the survival, growth, or reproduction of aphids that feed on it. Screening scores are based on the ability of the plant to decrease the rate of aphid reproduction. Plants are compared to resistant and susceptible check plants grown in the same experiment. Scores of 1 = susceptible, 3 = below average, 5 = average, 7 = above average, and 9 = exceptional tolerance. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

APHID ANTIXENOSIS. Aphid antixenosis is a property of a variety to reduce the feeding of aphids upon the plant, this is also known as nonpreference. Screening scores are based on the ability of the plant to decrease the rate of aphid reproduction. Plants are compared to resistant and susceptible check plants grown in the same experiment. Scores of 1 = susceptible plants covered with aphids, plants may show severe damage such as stunting and/or necrosis, equivalent or worse when compared to susceptible check, 3 = below average, plants show major damage such as stunting and/or foliar necrosis, 5 = moderately susceptible, 7 = above average, about 50 aphids on the plant, plant does not exhibit signs of plant stress, and 9 = exceptional tolerance, very few aphids on the plant, equivalent or better when compared to a resistant check. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

BACKCROSSING. Process in which a breeder crosses a donor parent variety possessing a desired trait or traits to a recurrent parent variety (which is agronomically superior but lacks the desired level or presence of one or more
traits) and then crosses the resultant progeny back to the recurrent parent one or more times. Backcrossing can be used to introduce one or more desired traits from one genetic background into another background that is lacking the desired traits.

**BREEDING.** The genetic manipulation of living organisms, including application of agricultural and/or biotechnological tools, methods and/or processes to create useful new distinct varieties.

**BU/A = Bushels per Acre.** The seed yield in bushels/acre is the actual yield of the grain at harvest.

**BROWN STEM ROT = BSR = Brown Stem Rot Tolerance.** This is a visual disease score from 1 to 9 comparing all genotypes in a given test. The score is based on leaf symptoms of yellowing, necrosis, and on inner stem rotting caused by *Phialophora gregata*. A score of 1 indicates severe symptoms of leaf yellowing and necrosis. Increasing visual scores from 2 to 8 indicate additional levels of tolerance, while a score of 9 indicates no symptoms. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

**BSRLF** = Brown Stem Rot disease rating based solely on leaf disease symptoms. This is a visual disease score from 1 to 9 comparing all genotypes in a given test. A score of 1 indicates severe leaf yellowing and necrosis. Increasing visual scores from 2 to 8 indicate additional levels of tolerance, while a score of 9 indicates no leaf symptoms. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

**BSRSTM = Brown Stem Rot disease rating based solely on stem disease symptoms.** This is a visual disease score from 1 to 9 comparing all genotypes in a given test. A score of 1 indicates severe necrosis on the inner stem tissues. Increasing visual scores from 2 to 8 indicate additional levels of tolerance, while a score of 9 indicates no inner stem symptoms. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.
CELL. Cell as used herein includes a plant cell, whether isolated, in tissue culture, or incorporated in a plant or plant part.

CERK = CERCOSPORA TOLERANCE. A fungal disease caused by Cercospora kukuchii which can be identified by mottled purple-to-orange discoloration of the uppermost leaves of the soybean plant. Infected seeds typically have a purple discoloration, which is commonly referred to as purple seed stain. Plants are visually scored from 1 to 9 comparing all genotypes in a given test. A score of 1 indicates severe discoloration of the leaves, while a score of 9 indicates no symptoms. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

CRDC = CHARCOAL ROT DISEASE. A fungal disease caused by Macrophomina phaseolina that is enhanced by hot and dry conditions, especially during reproductive growth stages. Tolerance score is based on observations of the comparative ability to tolerate drought and limit losses from charcoal rot infection among various soybean varieties. A score of 1 indicates severe charcoal rot on the roots and dark microsclerotia on the lower stem. Increasing visual scores from 2 to 8 indicate additional levels of tolerance, while a score of 9 indicates no lower stem and/or root rot. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

CHLORIDE SENSITIVITY. This is a measure of the chloride concentration in the plant tissue from 1 to 9. The higher the score the lower the concentration of chloride in the tissue measured. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

CW = Canopy Width. This is a visual observation of the canopy width which is scored from 1 to 9 comparing all genotypes in a given test. A score of 1 = very narrow, while a score of 9 = very bushy.

CNKR = STEM CANKER TOLERANCE. This is a visual disease score from 1 to 9 comparing all genotypes in a given field test. The score is based upon field reaction to the disease. Two causative agents have been identified,
Diaporthe phaseolorum var. caulivora, and Diaporthe phaseolorum var. meridionalis, which tend to impact different geographic regions, with D. phaseolorum var. caulivora identified as the causative agent for Northern stem canker, and D. phaseolorum var. meridionalis identified as the causative agent for Southern stem canker. CNKST indicates the tolerance score for Southern stem canker. A score of 1 indicates susceptibility to the disease, whereas a score of 9 indicates the line is resistant to the disease. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

CNKSG = STEM CANKER GENE. Resistance based on a specific gene that infers specific resistance or susceptibility to a specific race of Stem Canker. The score is based upon a reaction of toothpick inoculation with a race of stem canker. A score of 1 indicates severe stem canker lesions, similar to a known susceptible check variety, whereas a score of 9 indicates no disease symptoms, consistent with a known resistant check variety. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

COTYLEDON. A cotyledon is a type of seed leaf. The cotyledon contains the food storage tissues of the seed.

CROSS-POLLINATION. Fertilization by the union of two gametes from different plants.

DIPLOID. A cell or organism having two sets of chromosomes.

DM = DOWNY MILDEW. A fungal disease caused by Peronospora manshurica in soybean. Symptoms first appear on leaves, which can spread to pods without obvious external symptoms, and further spread to seed. Infected seed may have a dull white appearance. The tolerance score is based on observations of symptoms on the leaves of plants regarding leaf damage and/or level of infection. On a scale of 1 to 9, a score of 1 indicates severe symptoms, whereas a score of 9 indicates no disease symptoms. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.
ELITE VARIETY. A variety that is sufficiently homozygous and homogeneous to be used for commercial grain production. An elite variety may also be used in further breeding.

EMBRYO. The embryo is the small plant contained within a mature seed.

EMGSC = Emergence Score = Field Emergence. A score based upon speed and strength of emergence at sub-optimal conditions. Rating is done at the unifoliate to first trifoliate stages of growth. A score using a 1 to 9 scale is given, with 1 being the poorest and 9 the best. Scores of 1, 2, and 3 = degrees of unacceptable stands; slow growth and poor plant health. Scores of 4, 5, 6 = degrees of less than optimal stands; moderate growth and plant health. Scores of 7, 8, 9 = degrees of optimal stands; vigorous growth and plant health.

FEC = Iron-deficiency Chlorosis. Plants are scored 1 to 9 based on visual observations. A score of 1 indicates the plants are dead or dying from iron-deficiency chlorosis, a score of 5 means plants have intermediate health with some leaf yellowing, and a score of 9 means no stunting of the plants or yellowing of the leaves. Preliminary scores are reported as double digits, for example ‘55’ indicates a preliminary score of 5 on the scale of 1 to 9.

FEY = FROGEYE LEAF SPOT. This is a visual fungal disease score from 1 to 9 comparing all genotypes in a given experiment. The score is based upon the number and size of leaf lesions. A score of 1 indicates severe leaf necrosis spotting, whereas a score of 9 indicates no lesions. Preliminary scores are reported as double digits, for example ‘55’ indicates a preliminary score of 5 on the scale of 1 to 9.

FLOWER COLOR. Data values include: P = purple and W = white.

GENE SILENCING. The interruption or suppression of the expression of a nucleic acid sequence and/ or polypeptide sequence at the level of transcription or translation.

GENOTYPE. Refers to the genetic constitution of a cell or organism.

PLANT HABIT. This refers to the physical appearance of a plant. It can be determinate (Det), semi-determinate, intermediate, or indeterminate (Ind). In soybeans, indeterminate varieties are those in which stem growth is not limited
by formation of a reproductive structure (i.e., flowers, pods and seeds) and hence growth continues throughout flowering and during part of pod filling. The main stem will develop and set pods over a prolonged period under favorable conditions. In soybeans, determinate varieties are those in which stem growth ceases at flowering time. Most flowers develop simultaneously, and most pods fill at approximately the same time. The terms semi-determinate and intermediate are also used to describe plant habit and are defined in Bernard, R.L. (1972) "Two genes affecting stem termination in soybeans." Crop Science 12:235-239; Woodworth, C.M. (1932) "Genetics and breeding in the improvement of the soybean." Bull. Agric. Exp. Stn. (Illinois) 384:297-404; and Woodworth, C.M. (1933) "Genetics of the Soybean." J. Am. Soc. Agron. 25:36-51.

HAPLOID. A cell or organism having one set of the two sets of chromosomes in a diploid cell or organism.

HERBRES = Herbicide Resistance. This indicates that the plant is more tolerant to the herbicide shown than the level of herbicide tolerance exhibited by wild type plants. A designation of 'RR' indicates tolerance to glyphosate, a designation of 'GAT' indicates tolerance to glyphosate, and a designation of 'STS' indicates tolerance to sulfonylurea herbicides.

HGT = Plant Height. Plant height is taken from the top of the soil to the top pod of the plant and is measured in inches.

HILUM. This refers to the scar left on the seed which marks the place where the seed was attached to the pod prior to harvest. Hila Color data values include: BR = brown; TN = tan; Y = yellow; BL = black; IB = Imperfect Black; BF = buff. Tan hila may also be designated as imperfect yellow (IY).

HYPL = Hypocotyl length = Hypocotyl elongation. This score indicates the ability of the seed to emerge when planted 3" deep in sand pots and with a controlled temperature of 25°C. The number of plants that emerge each day are counted. Based on this data, each genotype is given a score from 1 to 9 based on its rate of emergence and the percent of emergence. A score of 1 indicates a very poor rate and percent of emergence, an intermediate score of 5 indicates
average ratings, and a score of 9 indicates an excellent rate and percent of emergence.

HYPOCOTYL. A hypocotyl is the portion of an embryo or seedling between the cotyledons and the root.

LDGSEV = Lodging Resistance = Harvest Standability. Lodging is rated on a scale of 1 to 9. A score of 1 indicates plants that are lying on the ground, a score of 5 indicates plants are leaning at a 45° angle in relation to the ground, and a score of 9 indicates erect plants.

LEAFLETS. These are parts of the plant shoot involved in the manufacture of food for the plant by the process of photosynthesis.

LINKAGE. Refers to a phenomenon wherein alleles on the same chromosome tend to segregate together more often than expected by chance if their transmission was independent.

LINKAGE DISEQUILIBRIUM. Refers to a phenomenon wherein alleles tend to remain together in linkage groups when segregating from parents to offspring, with a greater frequency than expected from their individual frequencies.

LLC = Oil with three percent or less linolenic acid is classified as low linolenic oil. Linolenic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

LLE = Linoleic Acid Percent. Linoleic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

LLN = Linolenic Acid Percent. Linolenic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

LOCUS. A defined segment of DNA.

PRM = PRMMAT= Predicted Relative Maturity = RM = Relative Maturity. Soybean maturities are divided into relative maturity groups (00, 0, I, II, III, IV,...X or 00, 0, 1, 2, 3,...10). Within a maturity group are sub-groups. A sub-group is a
tenth of a relative maturity group (for example, a relative maturity of 1.3 would indicate a group 1 and subgroup 3). Within narrow comparisons, the difference of a tenth of a relative maturity group equates very roughly to a day difference in maturity at harvest.

MAT ABS = ABSOLUTE MATURITY. This term is defined as the length of time from planting to complete physiological development (maturity). The period from planting until maturity is reached is measured in days, usually in comparison to one or more standard varieties. Plants are considered mature when 95% of the pods have reached their mature color.

MATURITY GROUP. This refers to an agreed-on industry division of groups of varieties, based on the zones in which they are adapted primarily according to day length or latitude. They consist of very long day length varieties (Groups 000, 00, 0), and extend to very short day length varieties (Groups VII, VIII, IX, X).

NARROW ROWS. Term indicates 7" and 15" row spacing.

NEI DISTANCE. A quantitative measure of percent similarity between two lines. Nei’s distance between lines A and B can be defined as $1 - \frac{2 \times \text{number alleles in common}}{\text{number alleles in A} + \text{number alleles in B}}$. For example, if lines A and B are the same for 95 out of 100 alleles, the Nei distance would be 0.05. If lines A and B are the same for 98 out of 100 alleles, the Nei distance would be 0.02. Free software for calculating Nei distance is available on the internet at multiple locations such as, e.g., evolution.genetics.washington.edu/phylip.html. See Nei & Li (1979) Proc Natl Acad Sci USA 76:5269-5273.

NUCLEIC ACID. An acidic, chainlike biological macromolecule consisting of multiple repeat units of phosphoric acid, sugar, and purine and pyrimidine bases.

OIL = OIL PERCENT = OIL (%). Soybean seeds contain a considerable amount of oil. Oil is measured by NIR spectrophotometry and is reported as a percentage basis.
OIL/MEAL TYPE. Designates varieties specially developed with the following oil traits: HLC = High Oleic oil; LLC = Low Linolenic (≤ 3% linolenic content); ULC = Ultra Low Linolenic oil (≤ 1% linolenic oil content); HSC = High Sucrose meal; LPA = Low Phytic Acid; LST = Low Saturate oil; Blank = Conventional variety/oil composition.

OLC = OLEIC ACID PERCENT. Oleic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

PEDIGREE DISTANCE. Relationship among generations based on their ancestral links as evidenced in pedigrees. May be measured by the distance of the pedigree from a given starting point in the ancestry.

PERCENT IDENTITY. Percent identity as used herein refers to the comparison of the homozygous alleles of two soybean varieties. Percent identity is determined by comparing a statistically significant number of the homozygous alleles of two developed varieties. For example, a percent identity of 90% between soybean variety 1 and soybean variety 2 means that the two varieties have the same allele at 90% of the loci used in the comparison.

PERCENT SIMILARITY. Percent similarity as used herein refers to the comparison of the homozygous alleles of a soybean variety such as XB14H11 with another plant, and if the homozygous allele of XB14H11 matches at least one of the alleles from the other plant, then they are scored as similar. Percent similarity is determined by comparing a statistically significant number of loci and recording the number of loci with similar alleles as a percentage. A percent similarity of 90% between XB14H11 and another plant means that XB14H11 matches at least one of the alleles of the other plant at 90% of the loci used in the comparison.

PLANT. As used herein, the term "plant" includes reference to an immature or mature whole plant, including a plant from which seed or grain or anthers have been removed. Seed or embryo that will produce the plant is also considered to be the plant.
PLANT PARTS. As used herein, the term "plant parts" includes leaves, stems, roots, root tips, anthers, seed, grain, embryos, pollen, ovules, flowers, cotyledon, hypocotyl, pod, flower, shoot, stalk, tissue, tissue cultures, cells and the like.

PLM or PALMITIC ACID PERCENT. Palmitic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

PMG infested soils. Soils containing Phytophthora sojae.

POD. This refers to the fruit of a soybean plant. It consists of the hull or shell (pericarp) and the soybean seeds. Pod Color data values include: BR = brown; TN = tan.

PRT or PHYTOPHTHORA FIELD TOLERANCE. Tolerance to Phytophthora root rot is rated on a scale of 1 to 9, with a score of 1 indicating the plants have no tolerance to Phytophthora, ranging to a score of 9 being the best or highest tolerance. PRTLAB indicates the tolerance was scored using plants in lab assay experiments. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

PHYTOPHTHORA RESISTANCE GENE (Rps). Various Phytophthora resistance genes are known and include but are not limited to: Rps1-a = resistance to races 1-2, 10-11, 13-8, 24; Rps1-c = resistance to races 1-3, 6-11, 13, 15, 17, 21, 23, 24, 26, 28-30, 32, 34, 36; Rps1-k = resistance to races 1-11, 13-15, 17, 18, 21-24, 26, 36, 37; Rps3-a = resistance to races 1-5, 8, 9, 11, 13, 14, 16, 18, 23, 25, 28, 29, 31-35, 39-41, 43-45, 47-52, 54; Rps3-c = resistance to races 1-4, 10-16, 18-36, 38-54; Rps6 = resistance to races 1-4, 10, 12, 14-16, 18-21, 25, 28, 33-35; and, Rps8 = resistance to races 1-5, 9, 13-15, 21, 25, 29, 32. As reported in Table 1 "-" or "-" indicates that a specific gene for resistance has not been identified to date.

PRO = PROTN = PROTN (%) = PROTEIN PERCENT. Soybean seeds contain a considerable amount of protein. Protein is generally measured by NIR spectrophotometry, and is reported as a percent on a dry weight basis.
PUBESCENCE. This refers to a covering of very fine hairs closely arranged on the leaves, stems and pods of the soybean plant. Pubescence color data values include: L = Light Tawny; T = Tawny; G = Gray.


R180 = Stearic acid percentage. Percentage of stearic acid as determined using methods described in Reske et al. (1997) JAOCS 74:989-998.


R182 = Linoleic acid percentage. Percentage of linoleic acid as determined using methods described in Reske et al. (1997) JAOCS 74:989-998.


RESISTANCE. As used herein, resistance is synonymous with tolerance and is used to describe the ability of a plant to withstand exposure to an insect, disease, herbicide, environmental stress, or other condition. A resistant plant variety will be able to better withstand the insect, disease pathogen, herbicide, environmental stress, or other condition as compared to a non-resistant or wild-type variety.

RKI = ROOT-KNOT NEMATODE, Southern. Southern root knot nematode, *Meloidogyne incognita*, is a plant parasite that can cause major damage. Resistance is visually scored on a range from 1 to 9 comparing all genotypes in a given experiment. The score is determined by digging plants to visually score the roots for presence or absence of galling. A score of 1 indicates large severe galling covering most of the root system which results in pre-mature death from decomposition of the root system (susceptible). A score of 9 indicates that there is no galling of the roots (resistant). Preliminary scores are reported as double digits, for example ‘55’ indicates a preliminary score of 5 on the scale of 1 to 9.
RKA = ROOT-KNOT NEMATODE, Peanut. Peanut root knot nematode, *Meloidogyne arenaria*, is a plant parasite that can cause major damage. Resistance is visually scored on a range from 1 to 9 comparing all genotypes in a given experiment. This is a visual disease score from 1 to 9 comparing all genotypes in a given experiment. The score is determined by digging plants to score the roots for presence or absence of galling. A score of 1 indicates large severe galling covering most of the root system which results in pre-mature death from decomposition of the root system (susceptible). A score of 9 indicates that there is no galling of the roots (resistant). Preliminary scores are reported as double digits, for example ‘55’ indicates a preliminary score of 5 on the scale of 1 to 9.

SCN = SOYBEAN CYST NEMATODE RESISTANCE = Cyst Nematode Resistance. The score is based on resistance to a particular race of soybean cyst nematode (*Heterodera glycines*), such as race 1, 2, 3, 5 or 14. Scores are from 1 to 9 and indicate visual observations of resistance as compared to other genotypes in the test. A score of 1 indicates nematodes are able to infect the plant and cause yield loss, while a score of 9 indicates SCN resistance. Preliminary scores are reported as double digits, for example ‘55’ indicates a preliminary score of 5 on the scale of 1 to 9.

SCN Resistance Source. There are three typical sources of genetic resistance to SCN: PI88788, PI548402 (also known as Peking), and PI437654 (also known as Hartwig).

SCN infected soils. Soils containing soybean cyst nematode.

SD VIG or Seedling Vigor. The score is based on the speed of emergence of the plants within a plot relative to other plots within an experiment. A score of 1 indicates no plants have expanded first leaves, while a score of 9 indicates that 90% of plants growing have expanded first leaves.

SDS or SUDDEN DEATH SYNDROME. SDS is caused by the fungal pathogen formerly known as *Fusarium solani f.sp. glycines*, which is currently known as *Fusarium virguliforme* (see, e.g., Aoki et al. (2003) Mycologia 95:660-684). Tolerance to Sudden Death Syndrome is rated on a scale of 1 to 9, with a
score of 1 being very susceptible ranging up to a score of 9 being tolerant. Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

SEED COAT LUSTER. Data values include D = dull; S = shiny.

SEED SIZE SCORE. This is a measure of the seed size from 1 to 9. The higher the score, the smaller the seed size measured.

SPLB = S/LB= Seeds per Pound. Soybean seeds vary in seed size, therefore, the number of seeds required to make up one pound also varies. This affects the pounds of seed required to plant a given area, and can also impact end uses.

SHATTR or Shattering. This refers to the amount of pod dehiscence prior to harvest. Pod dehiscence involves seeds falling from the pods to the soil. This is a visual score from 1 to 9 comparing all genotypes within a given test. A score of 1 indicates 100% of the pods are opened, while a score of 9 means pods have not opened and no seeds have fallen out.

SHOOTS. These are a portion of the body of the plant. They consist of stems, petioles and leaves.

STC or Stearic Acid Percent. Stearic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

SUBLINE. Although XB14H11 contains substantially fixed genetics, and is phenotypically uniform and with no off-types expected, there still remains a small proportion of segregating loci either within individuals or within the population as a whole. A breeder of ordinary skill in the art may fix these loci by making them more uniform in order to optimize the performance of the variety. Examples of this type of approach are described in the "breeding bias" methods described in U.S. Patent No. 5,437,697 and/or US2005/0071901 may be utilized by a breeder of ordinary skill in the art to further purify the variety in order to increase one or more aspects of its performance.

WHMD or WHITE MOLD TOLERANCE. This is a fungal disease caused by Sclerotinia sclerotiorum that creates mycelial growth and death of plants.
Tolerance to white mold is scored from 1 to 9 by visually comparing all genotypes in a given test. A score of 1 indicates complete death of the experimental unit while a score of 9 indicates no symptoms. Preliminary scores are reported as double digits, for example ‘55’ indicates a preliminary score of 5 on the scale of 1 to 9.

VARIETY. A substantially homozygous soybean line and minor modifications thereof that retain the overall genetics of the soybean line including but not limited to a subline, a locus conversion, a mutation, a transgenic, or a somaclonal variant. Variety includes seeds, plants, plant parts, and/or seed parts of the instant soybean line.

HIGH YIELD ENVIRONMENTS. Areas which lack normal stress, typically having sufficient rainfall, water drainage, low disease pressure, and low weed pressure.

TOUGH ENVIRONMENTS. Areas which have stress challenges, opposite of a high yield environment.

DETAILED DESCRIPTION

Soybean variety XB14H11 has shown uniformity and stability for all traits, as described in the following variety description information. Soybean variety XB14H11 was developed from a cross using EX21Q04 as a female parent with 90M60 as a male parent. Variety XB14H11 is an F2-derived line which was advanced to the F2 generation by modified single-seed descent. It has been self-pollinated a sufficient number of generations, with careful attention to uniformity of plant type to ensure a sufficient level of homozygosity and phenotypic stability. The variety has been increased with continued observation for uniformity. Variety XB14H11 is a uniform and stable variety. XB14H11 has valuable traits such as high yield for maturity, resistance to glyphosate, and resistance to Phytophthora megasperma, among others as shown in Tables 1 and 2.

A description of soybean variety XB14H11 is provided in Table 1. Traits reported are average values for all locations and years or samples measured.
Preliminary scores are reported as double digits, for example '55' indicates a preliminary score of 5 on the scale of 1 to 9.

Soybean variety XB14H11, being substantially homozygous, can be reproduced by planting seeds of the variety, growing the resulting soybean plants under self-pollinating or sib-pollinating conditions, and harvesting the resulting seed, using techniques familiar to the agricultural arts. Development of soybean variety XB14H11 is shown in the breeding history summary in Table 4.

Performance Examples of XB14H11

As shown in Table 2, the traits and characteristics of soybean variety XB14H11 are given in paired comparisons with other varieties. Traits reported are mean values for all locations and years where paired comparison data was obtained.

FURTHER EMBODIMENTS

Genetic Marker Profile

In addition to phenotypic observations, a plant can also be identified by its genotype. The genotype of a plant can be characterized through a genetic marker profile which can identify plants of the same variety or a related variety, or which can be used to determine or validate a pedigree. Genetic marker profiles can be obtained by techniques such as restriction fragment length polymorphisms (RFLPs), randomly amplified polymorphic DNAs (RAPDs), arbitrarily primed polymerase chain reaction (AP-PCR), DNA amplification fingerprinting (DAF), sequence characterized amplified regions (SCARs), amplified fragment length polymorphisms (AFLPs), simple sequence repeats (SSRs) also referred to as microsatellites, or single nucleotide polymorphisms (SNPs). For example, see Cregan et al. (1999) "An Integrated Genetic Linkage Map of the Soybean Genome" Crop Science 39:1464-1490, and Berry et al. (2003) "Assessing Probability of Ancestry Using Simple Sequence Repeat Profiles: Applications to Maize Inbred Lines and Soybean Varieties" Genetics 165:331-342.
Methods of characterizing soybean variety XB14H11, or a variety comprising the morphological and physiological characteristics of soybean variety XB14H11, are provided. In one example a method comprising isolating nucleic acids from a plant, a plant part, or a seed of soybean variety XB14H11, analyzing said nucleic acids to produce data, and recording the data for XB14H11 is provided. In some examples, the data is recorded on a computer readable medium. In other examples, the methods may further comprise using the data for soybean crossing, selection or advancement decisions. Crossing includes any type of plant breeding crossing method, including but not limited to outcrossing, selfing, backcrossing, locus conversion, introgression and the like.

Particular markers used for these purposes are not limited to any particular set of markers, but are envisioned to include any type of marker and marker profile which provides a means of distinguishing varieties. For example, one set of publicly available markers which could be used to screen and identify variety XB14H11 is disclosed in Table 3. In another example, one method of comparison is to use only homozygous loci for XB14H11.

Primers and PCR protocols for assaying these and other markers are disclosed in Soybase (sponsored by the USDA Agricultural Research Service and Iowa State University) located on the world wide web at 129.186.26.94/SSR.html. In addition to being used for identification of soybean variety XB14H11, and plant parts and plant cells of variety XB14H11, the genetic profile may be used to identify a soybean plant produced through the use of XB14H11 or to verify a pedigree for progeny plants produced through the use of XB14H11. The genetic marker profile is also useful in breeding and developing backcross conversions.

The present invention comprises a soybean plant characterized by molecular and physiological data obtained from the representative sample of said variety deposited with the American Type Culture Collection (ATCC). Thus, plants, seeds, or parts thereof, having all or substantially all of the physiological and morphological characteristics of soybean variety XB14H11 are provided. Further provided is a soybean plant formed by the combination of the disclosed
soybean plant or plant cell with another soybean plant or cell and comprising the homozygous alleles of the variety. A soybean plant comprising all of the physiological and morphological characteristics of soybean variety XB14H11 can be combined with another soybean plant in a soybean breeding program. In some examples the other soybean plant comprises all of the physiological and morphological characteristics of soybean variety XB14H11.

In some examples, a plant, a plant part, or a seed of soybean variety XB14H11 is characterized by producing a molecular profile. A molecular profile includes but is not limited to one or more genotypic and/or phenotypic profile(s). A genotypic profile includes but is not limited to a marker profile, such as a genetic map, a linkage map, a trait marker profile, a SNP profile, an SSR profile, a genome-wide marker profile, a haplotype, and the like. A molecular profile may also be a nucleic acid sequence profile, and/or a physical map. A phenotypic profile includes but is not limited to a protein expression profile, a metabolic profile, an mRNA expression profile, and the like.

Means of performing genetic marker profiles using SSR polymorphisms are well known in the art. A marker system based on SSRs can be highly informative in linkage analysis relative to other marker systems in that multiple alleles may be present. Another advantage of this type of marker is that, through use of flanking primers, detection of SSRs can be achieved, for example, by using the polymerase chain reaction (PCR), thereby eliminating the need for labor-intensive Southern hybridization. PCR detection is done using two oligonucleotide primers flanking the polymorphic segment of repetitive DNA to amplify the SSR region.

Following amplification, markers can be scored by electrophoresis of the amplification products. Scoring of marker genotype is based on the size of the amplified fragment, which correlates to the number of base pairs of the fragment. While variation in the primer used or in laboratory procedures can affect the reported fragment size, relative values should remain constant regardless of the specific primer or laboratory used. When comparing varieties it is preferable if all SSR profiles are performed in the same lab.

The SSR profile of soybean plant XB14H11 can be used to identify plants comprising XB14H11 as a parent, since such plants will comprise the same homozygous alleles as XB14H11. Because the soybean variety is essentially homozygous at all relevant loci, most loci should have only one type of allele present. In contrast, a genetic marker profile of an F1 progeny should be the sum of those parents, e.g., if one parent was homozygous for allele X at a particular locus, and the other parent homozygous for allele Y at that locus, then the F1 progeny will be XY (heterozygous) at that locus. Subsequent generations of progeny produced by selection and breeding are expected to be of genotype XX (homozygous), YY (homozygous), or XY (heterozygous) for that locus position. When the F1 plant is selfed or sibbed for successive filial generations, the locus should be either X or Y for that position.

In addition, plants and plant parts substantially benefiting from the use of XB14H11 in their development, such as XB14H11 comprising a backcross conversion, transgene, or genetic sterility factor, may be identified by having a molecular marker profile with a high percent identity to XB14H11. Such a percent identity might be 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% identical to XB14H11.

The SSR profile of variety XB14H11 also can be used to identify essentially derived varieties and other progeny varieties developed from the use of XB14H11, as well as cells and other plant parts thereof. Plants of the invention include any plant having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% of the markers in the SSR profile, and that retain 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% of the physiological and morphological characteristics of variety XB14H11.
when grown under the same conditions. Such plants may be developed using the markers identified in WO 00/31964, U.S. Patent 6,162,967 and U.S. Patent 7,288,386. Progeny plants and plant parts produced using XB14H11 may be identified by having a molecular marker profile of at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.5% genetic contribution from soybean variety XB14H11, as measured by either percent identity or percent similarity. Such progeny may be further characterized as being within a pedigree distance of XB14H11, such as within 1, 2, 3, 4, or 5 or less cross-pollinations to a soybean plant other than XB14H11, or a plant that has XB14H11 as a progenitor. Unique molecular profiles may be identified with other molecular tools such as SNPs and RFLPs.

Introduction of a new trait or locus into XB14H11

Variety XB14H11 represents a new base genetic variety into which a new locus or trait may be introgressed. Direct transformation and backcrossing represent two important methods that can be used to accomplish such an introgression.

A backcross conversion of XB14H11 occurs when DNA sequences are introduced through backcrossing (Hallauer et al. in Corn and Corn Improvement, Sprague and Dudley, Third Ed. 1998) with XB14H11 utilized as the recurrent parent. Both naturally occurring and transgenic DNA sequences may be introduced through backcrossing techniques. A backcross conversion may produce a plant with a trait or locus conversion in at least two or more backcrosses, including at least 2 backcrosses, at least 3 backcrosses, at least 4 backcrosses, or more. Molecular marker assisted breeding or selection may be utilized to reduce the number of backcrosses necessary to achieve the backcross conversion. For example, see Openshaw et al., “Marker-assisted Selection in Backcross Breeding”. In: Proceedings Symposium of the Analysis of Molecular Data, August 1994, Crop Science
Society of America, Corvallis, OR, which demonstrated that a backcross conversion can be made in as few as two backcrosses.

The complexity of the backcross conversion method depends on the type of trait being transferred (a single gene or closely linked genes compared to unlinked genes), the level of expression of the trait, the type of inheritance (cytoplasmic or nuclear), dominant or recessive trait expression, and the types of parents included in the cross. It is understood by those of ordinary skill in the art that for single gene traits that are relatively easy to classify, the backcross method is effective and relatively easy to manage. (See Hallauer et al. in Corn and Corn Improvement, Sprague and Dudley, Third Ed. 1998). Desired traits that may be transferred through backcross conversion include, but are not limited to, sterility (nuclear and cytoplasmic), fertility restoration, nutritional enhancements, drought tolerance, nitrogen utilization, altered fatty acid profile, low phytate, industrial enhancements, disease resistance (bacterial, fungal, or viral), insect resistance, and herbicide resistance. In addition, a recombination site itself, such as an FRT site, Lox site, or other site specific integration site, may be inserted by backcrossing and utilized for direct insertion of one or more genes of interest into a specific plant variety. A single locus may contain several transgenes, such as a transgene for disease resistance and a transgene for herbicide resistance. The gene for herbicide resistance may be used as a selectable marker and/or as a phenotypic trait. A single locus conversion of site specific integration system allows for the integration of multiple genes at a known recombination site in the genome.

The backcross conversion may result from either the transfer of a dominant allele or a recessive allele. Selection of progeny containing the trait of interest can be accomplished by direct selection for a trait associated with a dominant allele. Transgenes transferred via backcrossing typically function as a dominant single gene trait and are relatively easy to classify. Selection of progeny for a trait that is transferred via a recessive allele requires growing and selfing the first backcross generation to determine which plants carry the recessive alleles. Recessive traits may require additional progeny testing in
successive backcross generations to determine the presence of the locus of interest. The last backcross generation is usually selfed to give pure breeding progeny for the trait(s) being transferred, although a backcross conversion with a stably introgressed trait may also be maintained by further backcrossing to the recurrent parent with subsequent selection for the trait.

Along with selection for the trait of interest, progeny are selected for the phenotype of the recurrent parent. The backcross is a form of inbreeding, and the features of the recurrent parent are automatically recovered after successive backcrosses. Poehlman suggests from one to four or more backcrosses, but as noted above, the number of backcrosses necessary can be reduced with the use of molecular markers (Poehlman et al., 1995) Breeding Field Crops, 4th Ed., Iowa State University Press, Ames, IA). Other factors, such as a genetically similar donor parent, may also reduce the number of backcrosses necessary. As noted by Poehlman, backcrossing is easiest for simply inherited, dominant, and easily recognized traits.

One process for adding or modifying a trait or locus in soybean variety XB14H11 comprises crossing XB14H11 plants grown from XB14H11 seed with plants of another soybean plant that comprises a desired trait lacking in XB14H11, selecting F1 progeny plants that possess the desired trait or locus to produce selected F1 progeny plants, crossing the selected progeny plants back to XB14H11 plants to produce backcross1 (BC1) progeny plants. The BC1F1 progeny plants that have the desired trait and the morphological characteristics of soybean variety XB14H11 are selected and backcrossed to XB14H11 to generate BC2F1 progeny plants. Additional backcrossing and selection of progeny plants with the desired trait will produce BC3F1, BC4F1, BC5F1, ...BCxF1 generations of plants. The backcross populations of XB14H11 may be further characterized as having the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions and/or may be characterized by percent similarity or identity to XB14H11 as determined by SSR or other molecular markers. The above method may be
utilized with fewer backcrosses in appropriate situations, such as when the donor parent is highly related or molecular markers are used in one or more selection steps. Desired traits that may be used include those nucleic acids known in the art, some of which are listed herein, that will affect traits through nucleic acid expression or inhibition. Desired loci also include the introgression of FRT, Lox, and/or other recombination sites for site specific integration. Desired loci further include QTLs, which may also affect a desired trait.

In addition, the above process and other similar processes described herein may be used to produce first generation progeny soybean seed by adding a step at the end of the process that comprises crossing XB14H11 with the introgressed trait or locus with a different soybean plant and harvesting the resultant first generation progeny soybean seed.

Transgenes and transformation methods provide means to engineer the genome of plants to contain and express heterologous genetic elements, including but not limited to foreign genetic elements, additional copies of endogenous elements, and/or modified versions of native or endogenous genetic elements, in order to alter at least one trait of a plant in a specific manner that would be difficult or impossible to obtain with traditional plant breeding alone. Any heterologous DNA sequence(s), whether from a different species or from the same species, which are inserted into the genome using transformation, backcrossing, or other methods known to one of skill in the art are referred to herein collectively as transgenes. The sequences are heterologous based on sequence source, location of integration, operably linked elements, or any combination thereof. One or more transgenes of interest can be introduced into soybean variety XB14H11. Transgenic variants of soybean variety XB14H11 plants, seeds, cells, and parts thereof or derived therefrom are provided. Transgenic variants of XB14H11 comprise the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions, and/or may be characterized or identified by percent similarity or identity to XB14H11 as determined by SSR or other molecular markers. In some
examples, transgenic variants of soybean variety XB14H11 are produced by introducing at least one transgene of interest into soybean variety XB14H11 by transforming XB14H11 with a polynucleotide comprising the transgene of interest. In other examples, transgenic variants of soybean variety XB14H11 are produced by introducing at least one transgene by introgressing the transgene into soybean variety XB14H11 by crossing.

In one example, a process for modifying soybean variety XB14H11 with the addition of a desired trait, said process comprising transforming a soybean plant of variety XB14H11 with a transgene that confers a desired trait is provided. Therefore, transgenic XB14H11 soybean cells, plants, plant parts, and seeds produced from this process are provided. In some examples, the desired trait may be one or more of herbicide resistance, insect resistance, disease resistance, decreased phytate, modified fatty acid profile, modified fatty acid content, carbohydrate metabolism, protein content, or oil content. The specific gene may be any known in the art or listed herein, including but not limited to a polynucleotide conferring resistance to imidazolinone, sulfonylurea, protoporphyrinogen oxidase (PPO) inhibitors, hydroxyphenyl pyruvate dioxygenase (HPPD) inhibitors, glyphosate, glufosinate, triazine, 2,4-dichlorophenoxyacetic acid (2,4-D), dicamba, or benzonitrile herbicides; a polynucleotide encoding a \textit{Bacillus thuringiensis} polypeptide, a polynucleotide encoding a phytase, a fatty acid desaturase (e.g., FAD-2, FAD-3), galactinol synthase, a raffinose synthetic enzyme; or a polynucleotide conferring resistance to soybean cyst nematode, brown stem rot, \textit{Phytophthora} root rot, soybean mosaic virus, sudden death syndrome, or other plant pathogen.

Numerous methods for plant transformation have been developed, including biological and physical plant transformation protocols. See, for example, Miki \textit{et al.}, "Procedures for Introducing Foreign DNA into Plants" in \textit{Methods in Plant Molecular Biology and Biotechnology}, Glick, B.R. and Thompson, J.E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 67-88; and Armstrong (1999) "The First Decade of Maize Transformation: A Review and Future Perspective" Maydica 44:101-109. In addition, expression vectors and \textit{in
vitro culture methods for plant cell or tissue transformation and regeneration of plants are available. See, for example, Gruber et al., "Vectors for Plant Transformation" in Methods in Plant Molecular Biology and Biotechnology, Glick, B.R. and Thompson, J.E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 89-119.

The most prevalent types of plant transformation methods involve the construction of an expression vector. Such a vector comprises a DNA sequence that contains a gene under the control of or operatively linked to a regulatory element, for example a promoter. The vector may contain one or more genes and one or more regulatory elements.

A genetic trait which has been engineered into the genome of a particular soybean plant may then be moved into the genome of another variety using traditional breeding techniques that are well known in the plant breeding arts. For example, a backcrossing approach is commonly used to move a transgene from a transformed soybean variety into an elite soybean variety, and the resulting backcross conversion plant would then contain the transgene(s).

Various genetic elements can be introduced into the plant genome using transformation. These elements include, but are not limited to genes; coding sequences; inducible, constitutive, and tissue specific promoters; enhancing sequences; and signal and targeting sequences.

Transgenic plants can be used to produce commercial quantities of a foreign protein. Thus, techniques for the selection and propagation of transformed plants, which are well understood in the art, yield a plurality of transgenic plants that are harvested in a conventional manner, and a heterologous protein then can be extracted from a tissue of interest or from total biomass. Protein extraction from plant biomass can be accomplished by known methods which are discussed, for example, by Heney and Orr (1981) Anal. Biochem. 114:92-6.

A genetic map can be generated that identifies the approximate chromosomal location of the integrated DNA molecule, for example via conventional restriction fragment length polymorphisms (RFLP), polymerase
chain reaction (PCR) analysis, simple sequence repeats (SSR), and single
nucleotide polymorphisms (SNP). For exemplary methodologies in this regard,
see Glick and Thompson, Methods in Plant Molecular Biology and

Wang et al. discuss "Large Scale Identification, Mapping and Genotyping
280:1077-1082, and similar capabilities are increasingly available for the
soybean genome. Map information concerning chromosomal location is useful
for proprietary protection of a subject transgenic plant. If unauthorized
propagation is undertaken and crosses made with other germplasm, the map of
the integration region can be compared to similar maps for suspect plants to
determine if the latter have a common parentage with the subject plant. Map
comparisons could involve hybridizations, RFLP, PCR, SSR, sequencing or
combinations thereof, all of which are conventional techniques. SNPs may also
be used alone or in combination with other techniques.

Likewise, plants can be genetically engineered to express various
phenotypes of agronomic interest. Through the transformation of soybean the
expression of genes can be altered to enhance disease resistance, insect
resistance, herbicide resistance, agronomic, grain quality, and other traits.
Transformation can also be used to insert DNA sequences which control or help
control male-sterility. DNA sequences native to soybean as well as non-native
DNA sequences can be transformed into soybean and used to alter levels of
native or non-native proteins. Various promoters, targeting sequences,
enhancing sequences, and other DNA sequences can be inserted into the
genome for the purpose of altering the expression of proteins. Reduction of the
activity of specific genes (also known as gene silencing or gene suppression) is
desirable for several aspects of genetic engineering in plants.

Many techniques for gene silencing are well known to one of skill in the
art, including but not limited to, knock-outs (such as by insertion of a
transposable element such as mu (Vicki Chandler, The Maize Handbook ch. 118
(Springer-Verlag 1994); antisense technology (see, e.g., Sheehy et al. (1988))

Exemplary nucleotide sequences that may be altered by genetic engineering include, but are not limited to, those categorized below.

1. Transgenes That Confer Resistance To Insects Or Disease And That Encode:

   (A) Plant disease resistance genes. Plant defenses are often activated by specific interaction between the product of a disease resistance gene (R) in the plant and the product of a corresponding avirulence (Avr) gene in the pathogen. A plant variety can be transformed with cloned resistance gene to engineer plants that are resistant to specific pathogen strains. See, for example Jones et al. (1994) Science 266: 789 (cloning of the tomato Cf-9 gene for resistance to Cladosporium fulvum); Martin et al. (1993) Science 262:1432 (tomato Pto gene for resistance to Pseudomonas syringae pv. tomato encodes a protein kinase); Mindrinos et al. (1994) Cell 78:1089 (Arabidopsis RPS2 gene for resistance to Pseudomonas syringae), McDowell & Woffenden (2003) Trends
Biotechnol. 21:178-83; and Toyoda et al. (2002) Transgenic Res. 11:567-82. A plant resistant to a disease is one that is more resistant to a pathogen as compared to the wild type plant.

(B) A *Bacillus thuringiensis* (*Bt*) protein, a derivative thereof or a synthetic polypeptide modeled thereon. See, for example, Geiser *et al.* (1986) Gene 48:109, who disclose the cloning and nucleotide sequence of a *Bt* delta-endotoxin gene. Moreover, DNA molecules encoding delta-endotoxin genes can be purchased from American Type Culture Collection (Rockville, MD), for example, under ATCC Accession Nos. 40098, 67136, 31995, and 31998. Other non-limiting examples of *Bacillus thuringiensis* transgenes being genetically engineered are given in the following patents and patent applications: U.S. Patents 5,188,960; 5,689,052; 5,880,275; 5,986,177; 7,105,332; 7,208,474; WO 91/14778; WO 99/31248; WO 01/12731; WO 99/24581; WO 97/40162; US2002/0151709; US2003/0177528; US2005/0138685; US/20070245427; US2007/0245428; US2006/0241042; US2008/0020964; US2008/0020968; US2008/0020967; US2008/0172762; US2008/0172762; and US2009/0005306.

(C) An insect-specific hormone or pheromone such as an ecdysteroid or juvenile hormone, a variant thereof, a mimic based thereon, or an agonist or antagonist thereof. See, for example, the disclosure by Hammock *et al.* (1990) Nature 344:458, of baculovirus expression of cloned juvenile hormone esterase, an inactivator of juvenile hormone.

(E) An enzyme responsible for a hyperaccumulation of a monoterpen, a sesquiterpene, a steroid, hydroxamic acid, a phenylpropanoid derivative, or another non-protein molecule with insecticidal activity.

(F) An enzyme involved in the modification, including the post-translational modification, of a biologically active molecule; for example, a glycolytic enzyme, a proteolytic enzyme, a lipolytic enzyme, a nuclease, a cyclase, a transaminase, an esterase, a hydrolase, a phosphatase, a kinase, a phosphorylase, a polymerase, an elastase, a chitinase and a glucanase, whether natural or synthetic. See WO 93/02197, which discloses the nucleotide sequence of a callase gene. DNA molecules which contain chitinase-encoding sequences can be obtained, for example, from the ATCC under Accession Nos. 39637 and 67152. See also Kramer et al. (1993) Insect Biochem. Molec. Biol. 23:691, who teach the nucleotide sequence of a cDNA encoding tobacco hookworm chitinase, and Kawalleck et al. (1993) Plant Mol. Biol. 21:673, who provide the nucleotide sequence of the parsley ubi4-2 polyubiquitin gene, and U.S. Patents 6,563,020; 7,145,060; and 7,087,810.

(G) A molecule that stimulates signal transduction. For example, see the disclosure by Botella et al. (1994) Plant Mol. Biol. 24:757, of nucleotide sequences for mung bean calmodulin cDNA clones, and Griess et al. (1994) Plant Physiol. 104:1467, who provide the nucleotide sequence of a maize calmodulin cDNA clone.


(I) A membrane permease, a channel former, or a channel blocker. For example, see the disclosure by Jaynes et al. (1993) Plant Sci. 89:43, of heterologous expression of a cecropin-beta lytic peptide analog to render transgenic tobacco plants resistant to Pseudomonas solanacearum.

(J) A viral-invasive protein or a complex toxin derived therefrom. For example, the accumulation of viral coat proteins in transformed plant cells
imps resistance to viral infection and/or disease development effected by the
virus from which the coat protein gene is derived, as well as by related viruses.
resistance has been conferred upon transformed plants against alfalfa mosaic
virus, cucumber mosaic virus, tobacco streak virus, potato virus X, potato virus Y,
tobacco etch virus, tobacco rattle virus, and tobacco mosaic virus.

(K) An insect-specific antibody or an immunotoxin derived therefrom.
Thus, an antibody targeted to a critical metabolic function in the insect gut would
inactivate an affected enzyme, killing the insect. Cf. Taylor et al., Abstract #497,
Seventh Int’l Symposium on Molecular Plant-Microbe Interactions (Edinburgh,
Scotland, 1994) (enzymatic inactivation in transgenic tobacco via production of
single-chain antibody fragments).

(L) A virus-specific antibody. See, for example, Tavladoraki et al.
(1993) Nature 366:469, who show that transgenic plants expressing recombinant
antibody genes are protected from virus attack.

(M) A developmental-arrestive protein produced in nature by a
pathogen or a parasite. Thus, fungal endo alpha-1,4-D-polygalacturonases
facilitate fungal colonization and plant nutrient release by solubilizing plant cell
wall homo-alpha-1,4-D-galacturonase. See Lamb et al. (1992) Bio/Technology
10:1436. The cloning and characterization of a gene which encodes a bean
endopolygalacturonase-inhibiting protein is described by Toubart et al. (1992)
Plant J. 2:367.

(N) A developmental-arrestive protein produced in nature by a plant.
For example, Logemann et al. (1992) Bio/Technology 10:305, have shown that
transgenic plants expressing the barley ribosome-inactivating gene have an
increased resistance to fungal disease.

(O) Genes involved in the systemic acquired resistance (SAR)
Response and/or the pathogenesis related genes. Briggs (1995) Current Biology


(Q) Detoxification genes, such as for fumonisin, beauvericin, moniliformin, zearealenone, and their structurally related derivatives. For example, see U.S. Patents 5,716,820; 5,792,931; 5,798,255; 5,846,812; 6,083,736; 6,538,177; 6,388,171; and 6,812,380.

(R) Cystatin and cysteine proteinase inhibitors. See U.S. Patent 7,205,453.

(S) Defensin genes. See WO 03/000863 and U.S. Patents 6,911,577; 6,855,865; 6,777,592; and 7,238,781.


(U) Genes that confer resistance to Phytophthora Root Rot, such as Rps1, Rps1-a, Rps1-b, Rps1-c, Rps1-d, Rps1-e, Rps1-k, Rps2, Rps3-a, Rps3-b, Rps3-c, Rps4, Rps5, Rps6, Rps7, Rps8, and other Rps genes. See, for example, Shoemaker et al. “Phytophthora Root Rot Resistance Gene Mapping in Soybean”, Plant Genome IV Conference, San Diego, CA (1995).

(V) Genes that confer resistance to Brown Stem Rot, such as described in U.S. Patent 5,689,035.

2. Transgenes That Confer Resistance To A Herbicide, For Example:

(A) A herbicide that inhibits the growing point or meristem, such as an imidazolinone, or a sulfonylurea. Exemplary genes include mutant ALS and AHAS enzymes as described, for example, by Lee et al. (1988) EMBO J. 7:1241; and, Miki et al. (1990) Theor. Appl.Genet. 80:449, respectively. See also, U.S. Patents 5,605,011; 5,013,659; 5,141,870; 5,767,361; 5,731,180; 5,304,732;
4,761,373; 5,331,107; 5,928,937; and 5,378,824; US2007/0214515; and WO
96/33270.

(B) Glyphosate (resistance imparted by mutant 5-enolpyruvl-3-
phosphoshikimate synthase (EPSP) and aroA genes, respectively) and other
phosphono compounds such as glufosinate (phosphinothricin acetyl transferase
(PAT) and Streptomyces hygroscopicus phosphinothricin acetyl transferase (bar)
genes), and pyridinone or phenoxy propionic acids and cyclohexones (ACCcase
inhibitor-encoding genes). See, for example, U.S. Patent 4,940,835 to Shah et
al., which discloses the nucleotide sequence of a form of EPSPS which can
confer glyphosate resistance. U.S. Patent 5,627,061 to Barry et al. also
describes genes encoding EPSPS enzymes. See also U.S. Patents 6,566,587;
6,338,961; 6,248,876; 6,040,497; 5,804,425; 5,633,435; 5,145,783; 4,971,908;
5,312,910; 5,188,642; 4,940,835; 5,866,775; 6,225,114; 6,130,366; 5,310,667;
4,535,060; 4,769,061; 5,633,448; 5,510,471; RE 36,449; RE 37,287; and
5,491,288; and. EP1173580; WO 01/66704; EP1173581; and EP1173582.
Glyphosate resistance is also imparted to plants that express a gene that
encodes a glyphosate oxido-reductase enzyme as described more fully in U.S.
Patents 5,776,760 and 5,463,175, which are incorporated herein by reference for
this purpose. In addition, glyphosate resistance can be imparted to plants by the
overexpression of genes encoding glyphosate N-acetyltransferase. See, for
Patents 7,462,481 and 7,405,074. A DNA molecule encoding a mutant aroA
gene can be obtained under ATCC accession No. 39256, and the nucleotide
sequence of the mutant gene is disclosed in U.S. Patent 4,769,061 to Comai.
European Patent Application No. 0 333 033 to Kumada et al. and U.S. Patent
4,975,374 to Goodman et al. disclose nucleotide sequences of glutamine
synthetase genes which confer resistance to herbicides such as L-
phosphinothricin. The nucleotide sequence of a phosphinothricin-acetyl-
transferase gene is provided in European Patent No. 0 242 246 and 0 242 236 to
Leemans et al. De Greef et al. (1989) Bio/Technology 7:61 describe the
production of transgenic plants that express chimeric bar genes coding for
phosphinothricin acetyl transferase activity. See also, U.S. Patents 5,969,213; 5,489,520; 5,550,318; 5,874,265; 5,919,675; 5,561,236; 5,648,477; 5,646,024; 6,177,616; and 5,879,903. Exemplary genes conferring resistance to phenoxy proprionic acids and cyclohexones, such as sethoxydim and haloxyfop, are the Acc1-S1, Acc1-S2, and Acc1-S3 genes described by Marshall et al. (1992) Theor. Appl. Genet. 83:435.

(C) A herbicide that inhibits photosynthesis, such as a triazine (psbA and gs+ genes) and a benzonitrile (nitrilase gene). Przibilla et al. (1991) Plant Cell 3:169, describe the transformation of Chlamydomonas with plasmids encoding mutant psbA genes. Nucleotide sequences for nitrilase genes are disclosed in U.S. Patent 4,810,648 to Stalker, and DNA molecules containing these genes are available under ATCC Accession Nos. 53435, 67441, and 67442. Cloning and expression of DNA coding for a glutathione S-transferase is described by Hayes et al. (1992) Biochem. J. 285:173.

(D) Acetohydroxy acid synthase, which has been found to make plants that express this enzyme resistant to multiple types of herbicides, has been introduced into a variety of plants (see, e.g., Hattori et al. (1995) Mol Gen Genet 246:419). Other genes that confer resistance to herbicides include: a gene encoding a chimeric protein of rat cytochrome P4507A1 and yeast NADPH-cytochrome P450 oxidoreductase (Shiota et al. (1994) Plant Physiol 106:17), genes for glutathione reductase and superoxide dismutase (Aono et al. (1995) Plant Cell Physiol 36:1687), and genes for various phosphotransferases (Datta et al. (1992) Plant Mol Biol 20:619).

(E) Protoporphyrinogen oxidase (protox) is necessary for the production of chlorophyll, which is necessary for all plant survival. The protox enzyme serves as the target for a variety of herbicidal compounds. These herbicides also inhibit growth of all the different species of plants present, causing their total destruction. The development of plants containing altered protox activity which are resistant to these herbicides are described in U.S. Patents 6,288,306; 6,282,837; and 5,767,373; and WO 01/12825.
3. Transgenes That Confer Or Contribute To a Grain And/Or Seed Characteristic, Such As:

   (A) Fatty acid profile(s), for example, by
       
       
       (2) Elevating oleic acid via FAD-2 gene modification and/or decreasing linolenic acid via FAD-3 gene modification (see U.S. Patents 6,063,947; 6,323,392; 6,372,965; and WO 93/11245).
       
       (3) Altering conjugated linolenic or linoleic acid content, such as in WO 01/12800.
       
       (4) Altering LEC1, AGP, Dek1, Superal1, mit1ps, various lpa genes such as lpa1, lpa3, hpt or hggt. For example, see WO 02/42424; WO 98/22604; WO 03/011015; U.S. Patents 6,423,886; 6,197,561; and, 6,825,397; US2003/0079247; US2003/0204870; WO 02/057439; WO 03/011015; and Rivera-Madrid et al. (1995) Proc. Natl. Acad. Sci. 92:5620-5624.

   B) Altered phosphorus content, for example, by:
       
       (1) Introduction of a phytase-encoding gene would enhance breakdown of phytate, adding more free phosphate to the transformed plant. For example, see Van Hartingsveldt et al. (1993) Gene 127:87, for a disclosure of the nucleotide sequence of an Aspergillus niger phytase gene.
       
       (2) Modulating a gene that reduces phytate content. In maize, this, for example, could be accomplished, by cloning and then re-introducing DNA associated with one or more of the alleles, such as the LPA alleles, identified in maize mutants characterized by low levels of phytic acid, such as in WO 05/113778; and/or by altering inositol kinase activity as in WO 02/059324; U.S. Patent 7.067,720; WO 03/027243; US2003/0079247; WO 99/05298; U.S. Patents 6,197,561; 6,291,224; and 6,391,348; WO 98/45448; WO 99/55882; and WO 01/04147.
       
       (C) Altered carbohydrates, for example, by altering a gene for an
enzyme that affects the branching pattern of starch or, a gene altering thioredoxin such as NTR and/or TRX (see U.S. Patent 6,531) and/or a gamma zein knockout or mutant such as cs27, or TUSC7, or en27 (See U.S. Patent 6,858,778; US2005/0160488; and US2005/0204418). See Shiroza et al. (1988) J. Bacteriol. 170:810 (nucleotide sequence of Streptococcus mutans fructosyltransferase gene); Steinmetz et al. (1985) Mol. Gen. Genet. 200:220 (nucleotide sequence of Bacillus subtilis levansucrase gene); Pen et al. (1992) Bio/Technology 10:292 (production of transgenic plants that express Bacillus licheniformis alpha-amylase); Elliot et al. (1993) Plant Mol. Biol. 21:515 (nucleotide sequences of tomato invertase genes); Søgaard et al. (1993) J. Biol. Chem. 268:22480 (site-directed mutagenesis of barley alpha-amylase gene); Fisher et al. (1993) Plant Physiol. 102:1045 (maize endosperm starch branching enzyme II); WO 99/10498 (improved digestibility and/or starch extraction through modification of UDP-D-xylose 4-epimerase, Fragile 1 and 2, Ref1, HCHL, C4H); and, U.S. Patent 6,232,529 (method of producing high oil seed by modification of starch levels (AGP). The fatty acid modification genes mentioned herein may also be used to affect starch content and/or composition through the interrelationship of the starch and oil pathways.

(D) Altered antioxidant content or composition, such as alteration of tocopherol or tocotrienols. For example, see U.S. Patents 6,787,683; 7,154,029; and WO 00/68393 involving the manipulation of antioxidant levels, and WO 03/082899 through alteration of a homogentisate geranyl geranyl transferase (hggf).

(E) Altered essential seed amino acids. For example, see U.S. Patent 6,127,600 (method of increasing accumulation of essential amino acids in seeds); U.S. Patent 6,080,913 (binary methods of increasing accumulation of essential amino acids in seeds); U.S. Patent 5,990,389 (high lysine); WO 99/40209 (alteration of amino acid compositions in seeds); WO 99/29882 (methods for altering amino acid content of proteins); U.S. Patent 5,850,016 (alteration of amino acid compositions in seeds); WO 98/20133 (proteins with enhanced levels of essential amino acids); U.S. Patent 5,885,802 (high
methionine); U.S. Patent 5,885,801 (high threonine); U.S. Patent 6,664,445
(plant amino acid biosynthetic enzymes); U.S. Patent 6,459,019 (increased lysine
and threonine); U.S. Patent 6,441,274 (plant tryptophan synthase beta subunit);
U.S. Patent 6,346,403 (methionine metabolic enzymes); U.S. Patent 5,939,599
(high sulfur); U.S. Patent 5,912,414 (increased methionine); WO 98/56935 (plant
amino acid biosynthetic enzymes); WO 98/45458 (engineered seed protein
having higher percentage of essential amino acids); WO 98/42831 (increased
lysine); U.S. Patent 5,633,436 (increasing sulfur amino acid content); U.S. Patent
5,559,223 (synthetic storage proteins with defined structure containing
programmable levels of essential amino acids); WO 96/01905 (increased
threonine); WO 95/15392 (increased lysine); U.S. Patents 6,930,225; 7,179,955;
6,803,498; US2004/0068767; and WO 01/79516.

4. Genes that Control Male-sterility

There are several methods of conferring genetic male sterility available,
such as multiple mutant genes at separate locations within the genome that
confer male sterility, as disclosed in U.S. Patents 4,654,465 and 4,727,219 to
Brar et al., and chromosomal translocations as described by Patterson in U.S.
Patents 3,861,709 and 3,710,511. In addition to these methods, Albertsen et al.
U.S. Patent 5,432,068, describe a system of nuclear male sterility which
includes: identifying a gene which is critical to male fertility; silencing this native
gene which is critical to male fertility; removing the native promoter from the
essential male fertility gene and replacing it with an inducible promoter; inserting
this genetically engineered gene back into the plant; and thus creating a plant
that is male sterile because the inducible promoter is not "on" resulting in the
male fertility gene not being transcribed. Fertility is restored by inducing, or
turning "on", the promoter, which in turn allows the gene that confers male fertility
to be transcribed. Male sterile soybean lines and characterization are discussed
(A) Introduction of a deacetylase gene under the control of a tapetum-specific promoter and with the application of the chemical N-Ac-PPT (WO 01/29237).

(B) Introduction of various stamen-specific promoters (WO 92/13956 and WO 92/13957).


For additional examples of nuclear male and female sterility systems and genes, see also, U.S. Patents 5,859,341; 6,297,426; 5,478,369; 5,824,524; 5,850,014; and 6,265,640.

5. Polynucleotides comprising a site for site specific DNA recombination. This includes the introduction of at least one FRT site that may be used in the FLP/FRT system and/or a Lox site that may be used in the Cre/Lox system. For example, see Lyznik et al. (2003) Plant Cell Rep 21:925-932; and WO 99/25821, which are hereby incorporated by reference. Other systems that may be used include the Gin recombinase of phage Mu (Maeser et al. (1991) Mol Gen Genet 230:170-176); the Pin recombinase of E. coli (Enomoto et al. (1983) J Bacteriol 156:663-668); and the R/RS system of the pSR1 plasmid (Araki et al. (1992) J Mol Biol 182:191–203).

6. Genes that affect abiotic stress resistance (including but not limited to flowering, ear, and seed development, enhancement of nitrogen utilization efficiency, altered nitrogen responsiveness, drought resistance or tolerance, cold resistance or tolerance, and salt resistance or tolerance) and increased yield under stress. For example, see WO 00/73475 where water use efficiency is altered through alteration of malate; U.S. Patents 5,892,009; 5,965,705; 5,929,305; 5,891,859; 6,417,428; 6,664,446; 6,706,866; 6,717,034; and 6,801,104; WO 00/060089; WO 01/026459; WO 00/1035725; WO 01/034726; WO 01/035727; WO 00/1036444; WO 01/036597; WO 01/036598; WO 00/2015675; WO 02/017430; WO 02/077185; WO 02/079403; WO 03/013227;
WO 03/013228; WO 03/014327; WO 04/031349; WO 04/076638; WO 98/09521; and WO 99/38977 describing genes, including CBF genes and transcription factors effective in mitigating the negative effects of freezing, high salinity, and drought on plants, as well as conferring other positive effects on plant phenotype; US2004/0148654 and WO 01/36596 where abscisic acid is altered in plants resulting in improved plant phenotype such as increased yield and/or increased tolerance to abiotic stress; WO 00/006341, WO 04/090143, U.S. Patents 7,531,723, and 6,992,237 where cytokinin expression is modified resulting in plants with increased stress tolerance, such as drought tolerance, and/or increased yield. Also see WO 02/02776, WO 03/052063, JP2002281975, U.S. Patent 6,084,153, WO 01/64898, U.S. Patent 6,177,275, and U.S. Patent 6,107,547 (enhancement of nitrogen utilization and altered nitrogen responsiveness). For ethylene alteration, see US2004/0128719, US2003/0166197, and WO 00/32761. For plant transcription factors or transcriptional regulators of abiotic stress, see e.g. US2004/0098764 or US2004/0078852.

Other genes and transcription factors that affect plant growth and agronomic traits such as yield, flowering, plant growth, and/or plant structure, can be introduced or introgressed into plants, see e.g., WO 97/49811 (LHY), WO 98/56918 (ESD4), WO 97/10339, and U.S. Patent 6,573,430 (TFL), U.S. Patent 6,713,663 (FT), WO 96/14414 (CON), WO 96/38560, WO 01/21822 (VRN1), WO 00/44918 (VRN2), WO 99/49064 (GI), WO 00/46358 (FRI), WO 97/29123, U.S. Patent 6,794,560, U.S. Patent 6,307,126 (GAI), WO 99/09174 (D8 and Rht), and WO 04/076638 and WO 04/031349 (transcription factors).

Development of Soybean Sublines

Sublines of XB14H11 may also be developed and are provided. Although XB14H11 contains substantially fixed genetics and is phenotypically uniform with no off-types expected, there still remains a small proportion of segregating loci either within individuals or within the population as a whole. Sublining provides the ability to select for these loci, which have no apparent morphological or
phenotypic effect on the plant characteristics, but may have an effect on overall yield. For example, the methods described in U.S. Patent 5,437,697 and US2005/0071901 may be utilized by a breeder of ordinary skill in the art to identify genetic loci that are associated with yield potential to further purify the variety in order to increase its yield. A breeder of ordinary skill in the art may fix agronomically important loci by making them homozygous in order to optimize the performance of the variety. The development of soybean sublines and the use of accelerated yield technology is a plant breeding technique.

Soybean varieties such as XB14H11 are typically developed for use in seed and grain production. However, soybean varieties such as XB14H11 also provide a source of breeding material that may be used to develop new soybean varieties. Plant breeding techniques known in the art and used in a soybean plant breeding program include, but are not limited to, recurrent selection, mass selection, bulk selection, backcrossing, pedigree breeding, open pollination breeding, restriction fragment length polymorphism enhanced selection, genetic marker enhanced selection, making double haploids, and transformation. Often combinations of these techniques are used. The development of soybean varieties in a plant breeding program requires, in general, the development and evaluation of homozygous varieties. There are many analytical methods available to evaluate a new variety. The oldest and most traditional method of analysis is the observation of phenotypic traits but genotypic analysis may also be used.

Methods for producing a soybean plant by crossing a first parent soybean plant with a second parent soybean plant wherein the first and/or second parent soybean plant is variety XB14H11 are provided. Also provided are methods for producing a soybean plant having substantially all of the morphological and physiological characteristics of variety XB14H11, by crossing a first parent soybean plant with a second parent soybean plant wherein the first and/or the second parent soybean plant is a plant having substantially all of the morphological and physiological characteristics of variety XB14H11 set forth in Table 1, as determined at the 5% significance level when grown in the same
environmental conditions. The other parent may be any soybean plant, such as a soybean plant that is part of a synthetic or natural population. Any such methods using soybean variety XB14H11 include but are not limited to: selfing, sibbing, backcrossing, mass selection, pedigree breeding, bulk selection, hybrid production, crossing to populations, and the like. These methods are well known in the art and some of the more commonly used breeding methods are described below. Descriptions of breeding methods can be found in one of several reference books (e.g., Allard, *Principles of Plant Breeding*, 1960; Simmonds, *Principles of Crop Improvement*, 1979; Fehr, "Breeding Methods for Cultivar Development", Chapter 7, *Soybean Improvement, Production and Uses*, 2nd ed., Wilcox editor, 1987).

Pedigree breeding starts with the crossing of two genotypes, such as XB14H11 or a soybean variety having all of the morphological and physiological characteristics of XB14H11, and another soybean variety having one or more desirable characteristics that is lacking or which complements XB14H11. If the two original parents do not provide all the desired characteristics, other sources can be included in the breeding population. In the pedigree method, superior plants are selfed and selected in successive filial generations. In the succeeding filial generations, the heterozygous allele condition gives way to the homozygous allele condition as a result of inbreeding. Typically in the pedigree method of breeding, five or more successive filial generations of selfing and selection are practiced: e.g., F1 \(\rightarrow\) F2; F2 \(\rightarrow\) F3; F3 \(\rightarrow\) F4; F4 \(\rightarrow\) F5; etc. In some examples, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more generations of selfing and selection are practiced. After a sufficient amount of inbreeding, successive filial generations will serve to increase seed of the developed variety. Typically, the developed variety comprises homozygous alleles at about 95% or more of its loci.

In addition to being used to create backcross conversion populations, backcrossing can also be used in combination with pedigree breeding. As discussed previously, backcrossing can be used to transfer one or more specifically desirable traits from one variety (the donor parent) to a developed variety (the recurrent parent), which has good overall agronomic characteristics.
yet may lack one or more other desirable traits. However, the same procedure can be used to move the progeny toward the genotype of the recurrent parent but at the same time retain many components of the non-recurrent parent by stopping the backcrossing at an early stage and proceeding with selfing and selection. For example, a soybean variety may be crossed with another variety to produce a first generation progeny plant. The first generation progeny plant may then be backcrossed to one of its parent varieties to create a BC1F1. Progeny are selfed and selected so that the newly developed variety has many of the attributes of the recurrent parent and yet several of the desired attributes of the donor parent. This approach leverages the value and strengths of both parents for use in new soybean varieties.

Therefore, in some examples a method of making a backcross conversion of soybean variety XB14H11, comprising the steps of crossing a plant of soybean variety XB14H11 or a soybean variety having all of the morphological and physiological characteristics of XB14H11 with a donor plant possessing a desired trait to introduce the desired trait, selecting an F1 progeny plant containing the desired trait, and backcrossing the selected F1 progeny plant to a plant of soybean variety XB14H11 are provided. This method may further comprise the step of obtaining a molecular marker profile of soybean variety XB14H11 and using the molecular marker profile to select for a progeny plant with the desired trait and the molecular marker profile of XB14H11. The molecular marker profile can comprise information from one or more markers. In one example the desired trait is a mutant gene or transgene present in the donor parent. In another example, the desired trait is a native trait in the donor parent.

Recurrent selection is a method used in a plant breeding program to improve a population of plants. Variety XB14H11, and/or a soybean variety having all of the morphological and physiological characteristics of XB14H11, is suitable for use in a recurrent selection program. The method entails individual plants cross pollinating with each other to form progeny. The progeny are grown and the superior progeny selected by any number of selection methods, which include individual plant, half-sib progeny, full-sib progeny, and selfed progeny.
The selected progeny are cross pollinated with each other to form progeny for another population. This population is planted and, again, superior plants are selected to cross pollinate with each other. Recurrent selection is a cyclical process and therefore can be repeated as many times as desired. The objective of recurrent selection is to improve the traits of a population. The improved population can then be used as a source of breeding material to obtain new varieties for commercial or breeding use, including the production of a synthetic cultivar. A synthetic cultivar is the resultant progeny formed by the intercrossing of several selected varieties.

Mass selection is a useful technique when used in conjunction with molecular marker enhanced selection. In mass selection, seeds from individuals are selected based on phenotype or genotype. These selected seeds are then bulked and used to grow the next generation. Bulk selection requires growing a population of plants in a bulk plot, allowing the plants to self-pollinate, harvesting the seed in bulk, and then using a sample of the seed harvested in bulk to plant the next generation. Also, instead of self pollination, directed pollination could be used as part of the breeding program.

Mutation breeding is another method of introducing new traits into soybean variety XB14H11 or a soybean variety having all of the morphological and physiological characteristics of XB14H11. Mutations that occur spontaneously or that are artificially induced can be useful sources of variability for a plant breeder. The goal of artificial mutagenesis is to increase the rate of mutation for a desired characteristic. Mutation rates can be increased by many different means including temperature, long-term seed storage, tissue culture conditions, radiation; such as X-rays, gamma rays (e.g., cobalt 60 or cesium 137), neutrons, (product of nuclear fission by uranium 235 in an atomic reactor), beta radiation (emitted from radioisotopes such as phosphorus 32 or carbon 14), ultraviolet radiation (preferably from 2500 to 2900nm), or chemical mutagens such as base analogues (5-bromo-uracil), related compounds (8-ethoxy caffeine), antibiotics (streptonigrin), alkylating agents (sulfur mustards, nitrogen mustards, epoxides, ethylenamines, sulfates, sulfonates, sulfones, lactones),
azide, hydroxylamine, nitrous acid, or acridines. Once a desired trait is observed through mutagenesis, the trait may then be incorporated into existing germplasm by traditional breeding techniques. Details of mutation breeding can be found in "Principles of Cultivar Development" Fehr, 1993, Macmillan Publishing Company. In addition, mutations created in other soybean plants may be used to produce a backcross conversion of XB14H11 that comprises such mutation.

Molecular markers, which include markers identified through the use of techniques such as isozyme electrophoresis, restriction fragment length polymorphisms (RFLPs), randomly amplified polymorphic DNAs (RAPDs), arbitrarily primed polymerase chain reaction (AP-PCR), DNA amplification fingerprinting (DAF), sequence characterized amplified regions (SCARs), amplified fragment length polymorphisms (AFLPs), simple sequence repeats (SSRs), and single nucleotide polymorphisms (SNPs), may be used in plant breeding methods utilizing XB14H11.


SSR technology is an efficient and practical marker technology; more marker loci can be routinely used and more alleles per marker locus can be found using SSRs in comparison to RFLPs. For example, Diwan and Cregan, described a highly polymorphic microsatellite loci in soybean with as many as 26 alleles (Diwan and Cregan (1997) Theor. Appl. Genet. 95:220-225). Single nucleotide polymorphisms (SNPs) may also be used to identify the unique genetic composition of the XB14H11, and any progeny varieties retaining or
derived from that unique genetic composition. Various molecular marker
techniques may be used in combination to enhance overall resolution.

Soybean DNA molecular marker linkage maps have been rapidly
constructed and widely implemented in genetic studies. One such study is
described in Cregan et al. (1999) Crop Science 39:1464-1490. Sequences and
PCR conditions of SSR loci in soybean, as well as the most current genetic map,
may be found in Soybase on the world wide web.

One use of molecular markers is quantitative trait loci (QTL) mapping.
QTL mapping is the use of markers which are known to be closely linked to
alleles that have measurable effects on a quantitative trait. Selection in the
breeding process is based upon the accumulation of markers linked to the
positive effecting alleles and/or the elimination of the markers linked to the
negative effecting alleles from the plant genome.

Molecular markers can also be used during the breeding process for the
selection of qualitative traits. For example, markers closely linked to alleles or
markers containing sequences within the actual alleles of interest can be used to
select plants that contain the alleles of interest during a backcrossing breeding
program. The markers can also be used to select for the genome of the
recurrent parent and against the genome of the donor parent. Using this
procedure can minimize the amount of genome from the donor parent that
remains in the selected plants. It can also be used to reduce the number of
crosses back to the recurrent parent needed in a backcrossing program. The
use of molecular markers in the selection process is often called genetic marker
enhanced selection.

Production of Double Haploids

The production of double haploids can also be used for the development
of plants with a homozygous phenotype in the breeding program. For example, a
soybean plant for which variety XB14H11 or a soybean variety having all of the
morphological and physiological characteristics of XB14H11 is a parent can be
used to produce double haploid plants. Double haploids are produced by the
doubling of a set of chromosomes (1N) from a heterozygous plant to produce a completely homozygous individual. For example, see Wan et al., "Efficient Production of Doubled Haploid Plants Through Colchicine Treatment of Anther-Derived Maize Callus" (1989) Theor Appl Genet 77:889-892, and US2003/0005479. This can be advantageous because the process omits the generations of selfing needed to obtain a homozygous plant from a heterozygous source.


In some examples a process for making a substantially homozygous XB14H11 progeny plant by producing or obtaining a seed from the cross of XB14H11 and another soybean plant and applying double haploid methods to the F1 seed or F1 plant or to any successive filial generation is provided. Based on studies in maize, and currently being conducted in soybean, such methods would decrease the number of generations required to produce a variety with similar genetics or characteristics to XB14H11. See Bernardo and Kahler (2001) Theor. Appl. Genet. 102:986-992.

In particular, a process of making seed retaining the molecular marker profile of soybean variety XB14H11 is contemplated, such process comprising obtaining or producing F1 seed for which soybean variety XB14H11 is a parent, inducing doubled haploids to create progeny without the occurrence of meiotic segregation, obtaining the molecular marker profile of soybean variety XB14H11, and selecting progeny that retain the molecular marker profile of XB14H11.

Methods using seeds, plants, cells, or plant parts of variety XB14H11 in tissue culture are provided, as are the cultures, plants, parts, cells, and/or seeds

Development of Soybean Variety XB14H11

The development of XB14H11 included traditional plant breeding and biotechnology techniques. Traditional plant breeding and biotechnology are both methods of genetic engineering that require a significant degree of human intervention to produce new and useful recombinations of genetic information.

Soybeans normally self pollinate in nature. In order to cross pollinate one soybean plant with another to produce progeny with a new combination of genetic traits, a method of cross pollination is employed. Cross pollination is known to those skilled in the art. Soybean cross pollination is achieved by emasculating a designated female plant and pollinating the female plant with pollen from the designated male parent. The following method was employed to
cross pollinate the soybean plants, but other methods can be used, or modified, as is known to those skilled in the art.

In some cases, the designated female soybean plant is emasculated. Emasculation is done before the anthers shed pollen to avoid self-pollination. Emasculation is done by selecting an immature bud on the designated female parent that was not opened and did not contain any viable pollen. The bud is artificially opened using sterile technique. The sepals are peeled off and the petals are pulled off by gently grabbing the petals with tweezers and wiggling in an upward motion until they release. Any remaining anthers are removed, leaving the stigma and style intact (i.e. the female organs). In other cases, the immature buds of the designated female plant are not emasculated, but are selected and opened at a stage where the anthers are too immature to shed any pollen. In both examples, a mature flower that is shedding pollen is selected from the designated male plant. The petals are removed from the mature flower that is shedding pollen. The pollen is gently applied to the stigma of the emasculated or non-emasculated bud of the female plant. In cases where non-emasculated buds are used, the male pollen is applied well before any intact anthers on the bud will shed pollen. The plant is tagged with the location of the fertilized bud. The fertilized bud is evaluated several times during the crossing season to confirm that a viable cross had been achieved, and to detect any selves that may have occurred using either emasculated or non-emasculated buds. Pods from the cross are hand harvested and the F1 seed from the pods were advanced to the F1 generation. Any F1 seeds produced can be advanced, typically 2-30 seeds are produced, but the number of seeds can be outside of this range and still be used to advance through the next stages of product development. For the F2 grow out, 300 to 800 seeds are typically planted.

Soybean variety XB14H11 was developed from a biparental cross using EX21Q04 as the female parent with 90M60 as the male parent. Variety XB14H11 is an F2-derived line which was advanced to the F2 generation by modified single-seed descent. It has been self-pollinated a sufficient number of generations, with careful attention to uniformity of plant type to ensure a sufficient
level of homozygosity and phenotypic stability. The variety has been increased
with continued observation for uniformity, and has been shown to be uniform and
stable for several generations.

Table 4 summarizes the development history of XB14H11. The
development of any given soybean variety can take from six to twelve years of
significant technical human intervention starting from the time the first cross is
made. Therefore, development of new varieties is a time-consuming process
that requires precise forward planning, efficient use of resources, and a minimum
of changes in direction. The development of a new variety typically involves the
coordinated effort of a team of approximately 50 or more scientists, including
plant breeders, molecular biologists, plant pathologists, entomologists,
agronomists, biochemists, bioinformaticians, market analysts, and automation
specialists. It is estimated that the development of a soybean variety typically
requires approximately 60,000 man hours of work, this effort can range from
about 30,000 to greater than 80,000 man hours. These efforts take place in
several international locations such as the United States (e.g., Iowa, Illinois,
Minnesota, and Ohio), Canada, Puerto Rico, and Chile, by taking advantage of
the climate in spring, summer, fall and winter of the various locations. Although
the development of a soybean variety takes several years, the actual number of
growing seasons used to develop the variety is greater than the number of years
reported due to the use of multiple growing locations. Accordingly, the
development of XB14H11 involved significant technical human intervention.

During the process of development, the plant populations as well as
individual plants are evaluated for general health, agronomics, and stability at
many stages. These evaluations typically include but are not limited to one or
more of the following characteristics: average maturity; range of maturity within a
population; general health of the population, for instance observation for
diseases and/or insects affecting leaves, stems, roots, and/or seed; plant
structure of the population, for instance slender, bushy, or intermediate plant
architecture; Standability or lodging; plant height; branching; podding, for
instance position and/or density; plant growth type, for example determinate,
semi-determinate, or indeterminate; flower color; pubescence color; shattering; response to weather or soils; and any other characteristics of interest.

During its development, soybean variety XB14H11 is assayed and/or planted in field trials and evaluated for a variety of traits and/or characteristics as compared to check varieties. The property(s) of appropriate check varieties include but are not limited to varieties with a similar relative maturity, varieties known to be susceptible to one or more particular diseases, insect, pathogen, herbicide or chemical, field condition, weather condition, soil type or condition, and/or crop management practice, varieties known to be tolerant or resistant to one or more particular diseases, insect, pathogen, herbicide or chemical, field condition, weather condition, soil type or condition, and/or crop management practice, varieties comprising one or more particular marker locus, and/or varieties derived from another appropriate variety or having a particular pedigree. Appropriate choice of check varieties for comparison assures an appropriate baseline and valid qualitative or quantitative assessment of any test varieties.

Throughout the course of the development of XB14H11, the plants can be tested for various traits including, but not limited to, glyphosate tolerance, phytophthora resistance, soybean cyst nematode resistance, white mold resistance, oil and protein profiles, marker loci, and relative maturity as described in the examples below.

The resulting line, XB14H11, is a high yielding variety. The development of this new soybean line was arduous and lengthy, and involved the cooperation and inventive skill of many scientists, including plant breeders, molecular biologists, plant pathologists, agronomists and biochemists, over the course of several years. The development of XB14H11 involved significant technical human intervention.

Industrial applicability

The seed of XB14H11, the plant produced from such seed, a progeny soybean plant produced from the crossing of this line, the resulting progeny seed, and various parts of the plant can be utilized in the production of an edible
protein product, vegetable oil, or other food products in accordance with known techniques. Soybean XB14H11 can also be used as a breeding line to develop new soybean varieties.

Examples

The following examples provide descriptions of several assays that can be used to characterize and/or select a soybean variety during one or more stages of variety development. Many other methods and assays are available and can be substituted for, or used in combination with, one or more of the examples provided herein. Tables 1, 2, and 4 each provide further information on soybean variety XB14H11, which results may be produced from at least one or more assays or methods described in the Examples.

Example 1. Soybean cyst nematode (SCN) phenotypic screening

Nematode Populations

Multiple populations of *Heterodera glycines* are maintained and increased on host plants. These populations are used to identify, purify, and characterize elite soybean varieties for resistance to soybean cyst nematode. The following races of soybean cyst nematode are maintained: Race 1 (Type HG 2.5), Race 2 (Type HG 1.2.5.7), Race 3 (Type HG 0 or Type HG 7), Race 5 (Type HG 2.5.7), and Race 14 (Type HG 1.3.6.7).

Eggs or juveniles at stage 2 (J) are used to inoculate host plants to increase their population. SCN infestation requires a minimum 35 days before the cysts reach maturity and can be used to inoculate soybean experiments. Cyst eggs/J2 inoculant is harvested through a series of washings, grindings, and screenings. Screens are used progressing from larger to smaller sizes, ending with a #500 screen.

Growth chamber screening of soybeans

Soybean plants are grown in cones. Cones are long containers approximately 12 inches long and 1.5 inches in diameter at the top (e.g., Ray Leach Cone-tainers™). The cone is designed to easily remove the root mass.
Three days after planting, an inoculum channel is made in the cone containing the experimental line by poking a 4 inch hole with a 10 ml pipette tip. One ml of inoculum is dispensed into the channel. The plants are watered manually for the duration of the test, with watering being moderately light during the first 3-5 days until J2 infects the roots.

Plants are scored approximately 28-35 days following inoculation when cyst reproduction on susceptible checks is sufficiently high. Plants are removed from their cones and the soil is removed from the roots by gently dipping the roots into a bucket of water. The plants are screened to identify native resistance to one or more of the five races of soybean cyst nematode inoculated using a combination of three methods (1) visual 9-6-1 score; (2) visual full count; and/or (3) microscope count score depending on the stage of the line when screened. In general, lines earlier in the development cycle (R1-R2) are screened by the visual 9-6-1 method, and lines that have progressed to later development phases (R3-R5) are screened by the visual full count and/or microscope count method(s).

**Visual 9-6-1 Scoring:** This method is a visual evaluation of the roots. Susceptible checks are first evaluated for the development of cysts on the root system. These counts are recorded and averaged across the experiment to determine the susceptible (SUS) check average. Roots from the test plants are then scored based on a comparison with the average of the susceptible checks as follows:

- 9 = 0-15% of the susceptible checks average
- 6 = 16-40% of the susceptible checks average
- 1 = ≥41% of the susceptible checks average

**Visual counts:** In this method, known checks are counted and reported in full. Observed cysts on the test plants are counted for comparison to the susceptible check plant scores. Cyst counts are converted to 1-9 scores based on the female index (FI). The female index (FI) is the percentage of the number of females cysts produced on each experimental line divided by the number produced on a standard susceptible soybean check, then the result is multiplied by 100. A low FI (<10) means that the SCN population is not able to reproduce
well on the test line, a high FI means that the SCN population is able to reproduce well on the test line.

**Microscope counts:** Cysts counts for SCN assays for checks and experimental line are determined by washing cysts from roots and counting the number of cysts under the microscope.

At about 28-35 days after inoculation, roots from the susceptible check controls are examined for yellow cysts to assess whether to begin the process of evaluating the test. Experimental lines are compared with known standard checks. Once adequate levels of cysts are detected on the check varieties, plants from the test lines are removed from cones one at a time. Soil is removed from roots by gently dipping the roots into a bucket of water. The root tissue is placed on a 850 micron (#20) pore sieve stacked over a 250 micron (#60) pore sieve and sprayed with a jet of water to dislodge cysts from the roots. Collected cysts are rinsed from the #60 sieve into a clean labeled cup using no more than 30 mls of additional water.

Once all the samples are collected, each sample is counted using a gridded counting dish under a stereo microscope. The number of cysts counted are recorded for each sample. Cyst counts on the test plants are converted to the 1-9 scoring scale based on the female index (FI) described above.

**Nematode Checks:**

The following exemplary SCN checks can be planted and used to monitor cyst development:

<table>
<thead>
<tr>
<th>Race 1</th>
<th>Race 2</th>
<th>Race 3</th>
<th>Race 5</th>
<th>Race 14</th>
</tr>
</thead>
<tbody>
<tr>
<td>92B12 RES</td>
<td>95M60 RES</td>
<td>9182 RES</td>
<td>92B12 RES</td>
<td>9182 RES</td>
</tr>
<tr>
<td>9281 SUS</td>
<td>9281 SUS</td>
<td>9281 SUS</td>
<td>9281 SUS</td>
<td>9281 SUS</td>
</tr>
<tr>
<td>9234 RES</td>
<td>PI437654 RES</td>
<td>9234 RES</td>
<td>9234 RES</td>
<td>9234 SUS</td>
</tr>
<tr>
<td>9392 SUS</td>
<td>9392 SUS</td>
<td>9392 SUS</td>
<td>9392 SUS</td>
<td>9392 SUS</td>
</tr>
<tr>
<td>91M12 MR</td>
<td>9234 MR</td>
<td>93B15 MR</td>
<td>91M12 SUS</td>
<td>93B15 MR</td>
</tr>
</tbody>
</table>

RES = Resistant; SUS = Susceptible; and, MR = Moderately Resistant

Example 2. Brown stem rot (BSR) phenotypic screening

60
Phenotypic resistance or tolerance to brown stem rot can be evaluated in the field. The fields are selected based on a strong history of BSR infection. Generally, BSR severity increases as soil pH decreases. BSR severity is generally greatest at pH 6.0 and declines as the pH increases. It has been observed that cool temperatures during the pod filling stage can also be a major factor in BSR development. Yield trial sites are valuable sources of good BSR ratings as well. Susceptible and resistant varieties are grown as checks.

The plants are observed in mid August for any stem browning or leaf chlorosis. BSR infection can be scored using stem and/or leaf tissues: (i) Split stem symptoms (BRSTM) and/or (ii) leaf scorch symptoms (BSRLF).

The scoring system for the BSRLF trait is an estimate of affected leaf area based on a visual assessment of incidence-by-severity for the plot. A 1-9 scale is used based on total leaf area of plot affected:

9 = no symptoms,
8 = slight symptoms (a few chlorotic spots can be found),
7 = about 15% affected leaf area,
6 = 30% affected leaf area,
5 = about 40% total leaf area affected,
4 = 50% affected leaf area,
3 = 60% affected leaf area,
2 = 70% affected leaf area,
1 = ≥ 80% affected leaf area).

Stems are periodically split to confirm if stem browning is present in plants showing leaf symptoms. As is known to those skilled in the art, there are two BSR pathogen types. Type A produces stem and leaf symptoms while Type B produces stem symptoms only. Split stems are scored based on the percent of brown nodes as follows:

9 = clean
8 = slight browning (1 or 2 nodes)
1 = nearly the entire plant with brown nodes
The pathology of the affected plants is evaluated to ensure that the symptoms are not being confused with sudden death syndrome.

The plots are scored approximately 2-3 times at 5-7 day intervals until the plot reached R7. R7 is a stage at the beginning of maturity, with seed in one or more pods that are physiologically mature.

Example 3. Phytophthora root rot (PMG)

*Phytophthora sojae* is maintained by refrigeration on agar. It is transferred to fresh agar plates to make inoculum for the test.

Test and check lines are grown in growth chambers under controlled light and controlled temperature conditions. The lines are inoculated at the seedling stage by injecting mycelium into the hypocotyl. The unclassified lines are incubated in conditions conducive for *Phytophthora* infection, and then evaluated when the known susceptible controls die. The plants can be inoculated with at least one of: *Phytophthora* race 4 (PMG04); *Phytophthora* race 7 (PMG07); and/or *Phytophthora* race 25 (PMG25).

Experiments are scored 2-3 days following inoculation, depending on the reaction of susceptible and resistant checks. Infection phenotypes are classified based on the number of seedlings alive divided by the total number of seedlings inoculated. For example,

- 9 = 9 of 9 plants alive and healthy
- 5 = 5 of 9 plants alive and healthy
- 1 = 1 or 0 of 9 plants alive and healthy
- M = no or poor germ (<5 seeds germinate)

Example 4. Glyphosate tolerance

Experimental lines and checks are treated 1X Round-up Power Max™ at a rate of 22oz/acre at the V1 growth stage, followed by a 2X Round up Power Max™ at a rate of 44oz/acre at the V3 growth stage plus 3 weeks. The V1 stage of the plant is the stage where the plant has one node on the main stem and the unifoliate leaves are fully developed and appear opposite each other. The V3
stage of the plant is the stage where the plant has three nodes on the main stem with fully developed leaves, beginning with the unifoliate node (i.e., node #1). Approximately 7-10 days after spraying, the number of dead plants/plot are counted and scored on a scale of 1-9 as follows:

9 = 100% of plants resistant  
8 = 90-99% of plants resistant  
7 = 80-89% of plants resistant  
6 = 70-79% of plants resistant  
5 = 60-69% of plants resistant  
4 = 50-59% of plants resistant  
3 = 40-49% of plants resistant  
2 = 30-39% of plants resistant  
1 = <30% of plants resistant

Example 5. Molecular analysis, including marker assisted selection (MAS)

As shown in Table 4, plants are analyzed at various times throughout the development of XB14H11 for specific alleles for various traits of interest (for example, soybean cyst nematode resistance, brown stem rot resistance, Phytophthora resistance, glyphosate resistance, and the like). Markers are detected using assays based on Taqman™ chemistry using fluorescently-labeled probe for allele discrimination. As is known to those skilled in the art, other methods of molecular analysis and marker assisted selection (MAS) could also be used.

Example 6. White mold (Sclerotinia sclerotiorum)

Sclerotia are maintained under refrigeration and subcultured on agar plates to produce inoculum when needed. Plants are grown in growth chambers under controlled light and controlled temperature conditions. Plants are inoculated with mycelium during the vegetative stage. The plants are then incubated in conditions conducive for white mold infection. Evaluation begins
when the known susceptible controls die. The experimental lines are scored and
given a 1-9 rating as follows:

9 = no symptoms or small necrotic lesion on the main stem, where the
inoculated petiole is attached.
7 = restricted fungal growth; lesion on the main stem <1" in length
5 = lesion >1" in length; plant has no sign of wilting
3 = plants starts to wilt or partially wilt; branches remain healthy
1= main stem wilting all the way to the growing point; whole plant wilting
and dying

Example 7. Oil and protein determination

Percent oil and protein in seed is determined using an Infratec™ 1241
grain analyzer using the USA-GIPSA official model pre-loaded into the
instrument software. The software also includes a library of data which is used
to interpolate the value of each measured component based on the NIR spectra
collected. Component measurements are based on calibration to a standard
reference method, see for example American Association of Cereal Chemist
methods for protein (method 46-11.02), oil (method 30-25.01), and moisture
(method 44-15.02) (AACC International. Approved Methods of Analysis, 11th Ed.
AACC International, St. Paul, MN, U.S.A.). Clean soybean seed is loaded in the
hopper, typically this is about one pound of seed. The instrument automatically
transfers ten sub-samples of seed from the hopper to the analysis chamber and
collects NIR data. The instrument calculates the average value for moisture, for
protein, and for oil, which are all reported as w/w%. The oil and protein data is
normalized and reported at 13% moisture.

Example 8. Relative maturity

Relative maturity (RM) is determined by assessing known varieties with a
known RM and generating a regression equation. Two traits are regressed in the
known varieties: Maturity Absolute (expressed in days); and, RM. Maturity
Absolute is the number of days from planting to physiological maturity.
Physiological maturity is defined as the date on which 95 percent of the pods are brown. The regression equation generated by these two traits using known varieties is used to predict the relative maturity of new lines. Typically, the X axis is expressed in maturity absolute days, and the Y axis is Relative Maturity. By using 4 or more known checks, an equation is deduced that produces a straight line. By substituting days absolute for the experimental line into the equation one can predict the relative maturity of the experimental line. The point where the Maturity Absolute date of the new line intersects the regression line determines the relative maturity of the new line. The relative maturity is based on multi-year and multi-location data. Relative maturity is preferred rather than absolute days because the difference in the number of days between several varieties can vary greatly from year-to-year, and from location-to-location. The relative maturity remains the same or is more stable across environments than the measure of absolute maturity.

Example 9. Field evaluation for Sudden Death Syndrome

Sudden death syndrome (SDS) is a disease caused by a soil borne fungus *Fusarium virguliforme* (previously known as *Fusarium solani* (Mart.) Sacc. f. sp. glycines). *Xanthomonas campestris* has also been proposed as a causative agent of SDS (see, e.g., de Farias Neto et al. (2006) Crop Sci 46:2547-2554; Scherm & Yang (1996) Phytopathol 86:642-649; and "Diseases of Soybean: Sudden Death Syndrome", online publication from Purdue University). The disease symptoms first appear on leaves as scattered, interveinal, chlorotic spots or blotches. The chlorotic areas may become necrotic or enlarge and coalesce, forming interveinal chlorotic streaks. Streaks eventually become necrotic, with only the midvein and major lateral veins remaining green. Affected field areas have a tan-brown cast, which may be the first evidence of disease. Root symptoms are characterized by deterioration of taproots, lateral roots, and nitrogen-fixing nodules. The cortex of affected taproots is a light gray-brown. The discoloration extends up the stem several nodes in the vascular tissue, but the pith remains white.
Soybean plants are scored using a 1-9 scale, wherein 1 indicates the most severe symptoms, and 9 indicates no symptoms:

9 = clean, no disease
8 = Up to 10% of plants showing mild symptoms
7 = Up to 20% plants showing mild symptoms
6 = up to 30% plants showing medium symptoms (considered the lowest ‘acceptable’ score)
5 = 40% or more of plants showing medium symptoms
4 = 50% or more plants showing medium to heavy symptoms
3,2,1 = 50% or more plants showing heavy symptoms, with increasing degrees of browning and/or necrosis or leaf loss.

Example 10. Iron Deficiency Chlorosis (IDC or FEC)

Iron Deficiency Chlorosis (IDC) evaluation is used to characterize and assign tolerance scores to experimental and commercial varieties. High carbonate levels in the soil can be a main cause of Iron Deficiency Chlorosis in soybean. Other stresses, such as cold temperature, SCN infection, saturated soils, or herbicide application may increase chlorosis. IDC symptoms range from slight yellowing of leaves to stunting, severe chlorosis, and sometimes death of plants in affected fields. Testing for tolerance to Iron Deficiency Chlorosis is performed during the summer using fields with a history of IDC. Plots are usually scored in late June to mid-July. The V3 stage (three nodes starting with the first unifoliate leaves) is usually the stage at which chlorosis symptoms are at their peak. Plants are scored on a scale of from 1-9 based on symptomology:

9 = All plants are normal green color
8 = A few plants are show very light chlorosis on 1 or 2 leaves
7 = < 50% of the plants show mild chlorosis (light green leaves)
6 = ≥ 50% of the plants show mild chlorosis, but no necrosis on leaves
5 = Most plants are light green to yellow, no necrosis seen on leaves. Most plants are stunted (50-75% of normal height).
4 = Most plants are yellow, necrosis seen on edges of less than half the leaves. Most plants are app. 50% of normal height
3 = Most plants are yellow, necrosis seen on most leaves. Most plants are app. 20-40% of normal height
2 = Most leaves are almost dead, most stems are still green. Plants are severely stunted (10-20% of normal height)
1 = Most plants are completely dead. The plants that are still alive are app. 10% of normal height, and have very little living tissue.

Example 11. Phytophthora Root Rot field tolerance


For testing, seed samples from experimental and check lines are not treated with any seed treatment. A known set of differential checks is used. One or more races of *Phytophthora* are chosen. Normally, at least Race 25 *Phytophthora sojae* is used. Experimental lines and checks are sown in vermiculite in trays that are inoculated with mycelium. The trays are moved outside to a location covered with 30% sunlight block netting.

Differential checks with low tolerance show symptoms 1-2 weeks after planting. Experimental lines are scored approximately three weeks after planting by removing the plants and root mass intact from the vermiculite. The vermiculite is removed by tapping the roots, without damaging the roots. All experimental entries are scored relative to the appearance of the root system of one or more
check variety(s) and the known performance chart score of each check. Scores are assigned on a scale of 1-9, and are relative to the differential checks and based upon total root mass, general appearance of plants and roots, and extent of necrosis.

1 = all plants die after emerging
2 = 50% less root mass than 9306
3 = equal to 9306
4 = 50% less root mass than Conrad, 25% more than 9306
5 = 25% less root mass than Conrad
6 = equal to Conrad
7 = equal to 92B38 and/or 93B67
8 = equal to 93B45
9 = equal to 9242

Example 12. Soybean varieties derived from soybean variety XB14H11
A. Use of soybean variety XB14H11 as a parent for biparental crosses

Soybean variety XB14H11 can be used as the female or the male parent in biparental crosses in order to develop new and valuable soybean varieties. Soybeans normally self pollinate in nature. Soybean cross pollination can be achieved by emasculating a designated female plant and pollinating the female plant with pollen from the designated male parent. Emasculation is done before the anthers shed pollen to avoid self-pollination. Immature buds on the designated female parent that are not open and do not contain any viable pollen are selected. The bud is artificially opened using sterile technique. The sepals are peeled off and the petals are pulled off by gently grabbing the petals with tweezers and wiggling in an upward motion until they release. Any remaining anthers are removed, leaving the stigma and style intact (i.e. the female organs).

In some cases, the immature buds of the designated female plant are not emasculated, but are selected and opened at a stage where the anthers are too immature to shed any pollen. In both examples, a mature flower that is shedding
pollen is selected from the designated male plant. The petals are removed from
the mature flower that is shedding pollen. The pollen is gently applied to the
stigma of the emasculated or non-emasculated bud of the female plant. In cases
where non-emasculated buds are used, the male pollen is applied well before
any intact anthers on the bud will shed pollen.

The plant is tagged with the location of the fertilized bud. The fertilized
bud is evaluated several times during the crossing season to confirm that a
viable cross had been achieved, and to detect any selves that may have occurred
using either emasculated or non-emasculated buds. Pods from the cross are
hand harvested and the F1 seed from the pods were advanced to the F1
generation. Any F1 seeds produced can be advanced, typically 2-30 seeds are
produced, but the number of seeds can be outside of this range and still be used
to advance through the next stages of product development. Soybean variety
XB14H11 has been used as a parent for biparental crossing. At least one
segregating population is expected to be produced to be used for further product
development phases and screening methods.

B. Sublining and sublines derived from soybean variety XB14H11

Sublines of XB14H11 may also be developed and are provided. Although
XB14H11 contains substantially fixed genetics and is phenotypically uniform with
no off-types observed or expected, the variety comprises some residual variation
due to a small proportion of segregating loci either within individuals or within the
population as a whole. Sublining selects for these loci, which have no
observable morphological or phenotypic effect on the plant characteristics, but
may have an effect on overall yield. For example, the methods described in U.S.
Patent 5,437,697 and US2005/0071901 may be utilized by a breeder of ordinary
skill in the art to identify genetic loci that are associated with yield potential to
further purify the variety in order to increase its yield.
DEPOSITS

Applicant made a deposit of seeds of Soybean Variety XB14H11 with the Patent Depository of the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110 USA on February 2, 2011, which was assigned ATCC Deposit No. PTA-11632. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. These deposits are not an admission that a deposit is required under Section 27(3) and 38.1(1) of the Patent Act.
All publications, patents and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains.

The foregoing invention has been described in detail by way of illustration and example for purposes of clarity and understanding. As is readily apparent to one skilled in the art, the foregoing are only some of the methods and compositions that illustrate the embodiments of the foregoing invention. It will be apparent to those of ordinary skill in the art that variations, changes, modifications and alterations may be applied to the compositions and/or methods described herein without departing from the true spirit, concept and scope of the invention.
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Claims

What is claimed is:

1. A plant cell from a soybean plant designated variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein soybean variety XB14H11 comprises a first transgene conferring glyphosate resistance.

2. The plant cell of claim 1, wherein the plant cell is a seed cell.

3. The plant cell of any one of claims 1 or 2, further comprising a second transgene.

4. A plant cell from a soybean plant, or a plant cell from a part of the soybean plant, wherein the soybean plant is produced by growing seed of soybean variety XB14H11, said seed having been deposited under ATCC Accession Number PTA-11632.

5. A plant cell from a soybean plant or soybean seed which is a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions.

6. A plant cell from a soybean plant or soybean seed which is a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11.
7. A plant cell from a plant tissue culture produced from protoplasts or regenerable cells from the plant cell of claim 1.

8. A plant cell from a descendant of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant comprises heterozygous alleles of variety XB14H11.

9. The plant cell of claim 8 wherein the plant cell is a seed cell.

10. A plant cell from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein XB14H11 comprises a first transgene conferring glyphosate resistance, and wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, and wherein the descendant or subline further comprises a second transgene.

11. A plant cell from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein XB14H11 comprises a first transgene conferring glyphosate resistance, and wherein the descendant or subline is essentially derived from soybean variety XB14H11, and wherein the descendant or subline further comprises a second transgene.

12. A plant cell from a soybean plant, or a plant cell from a part of the soybean plant, wherein the plant expresses all the physiological and morphological characteristics of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632.
13. An F1 plant cell from an F1 soybean plant, or a plant cell from a part of the F1 soybean plant, wherein the F1 soybean plant is the product of a cross between a first parent and a second parent, wherein either the first parent or second parent is a plant from soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, and wherein the F1 comprises heterozygous alleles of variety XB14H11.

14. Use of a soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to breed a soybean plant.

15. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to breed a soybean plant.

16. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to breed a soybean plant.

17. Use of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 as a recipient of a conversion locus.

18. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline
expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, as a recipient of a conversion locus.

19. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, as a recipient of a conversion locus.

20. Use of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to cross with another soybean plant.

21. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to cross with another soybean plant.

22. Use of a descendant or subline of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to cross with another soybean plant.

23. Use of soybean variety XB14H11 seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 and comprising a first transgene for glyphosate resistance, to introduce a second transgene.
24. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 and comprising a first transgene for glyphosate resistance, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to introduce a second transgene.

25. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632 and comprising a first transgene for glyphosate resistance, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to introduce a second transgene.

26. Use of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, for oil or protein production.

27. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, for oil or protein production.

28. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, for oil or protein production.
29. Use of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to grow a crop.

30. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to grow a crop.

31. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to grow a crop.

32. Crushed non-viable soybean seeds from soybean variety XB14H11, seeds of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632.

33. Crushed non-viable soybean seeds from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions.

34. Crushed non-viable soybean seeds from a descendant or subline of soybean variety XB14H11, soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the
descendant or subline is essentially derived from soybean variety XB14H11.

35. Use of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, to produce a genetic marker profile.

36. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline expresses the physiological and morphological characteristics of soybean variety XB14H11 listed in Table 1 as determined at the 5% significance level when grown under substantially similar environmental conditions, to produce a genetic marker profile.

37. Use of a descendant or subline of soybean variety XB14H11, seed of soybean variety XB14H11 having been deposited under ATCC Accession Number PTA-11632, wherein the descendant or subline is essentially derived from soybean variety XB14H11, to produce a genetic marker profile.

38. The use of any one of claims 35, 36 or 37 further comprising using the genetic marker profile for marker assisted selection.